

058543 - 065001

~~<120> IDENTIFICATION OF POLYNUCLEOTIDES
ENCODING NOVEL HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER
GENOME~~

<140> 08/881,227

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<212> DNA

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (56) \dots (931)$

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5 10 15

gat aat ata gaa aaa gat ttg aaa cat aaa atc caa ~~ata~~ ata acc gca 154
Asp Asn Ile Glu Lys Asp Leu Lys His Lys Ile Gln ~~Ile~~ Ile Thr Ala
20 25 30

caa acg cat aaa cgc ccc aaa cta gcc gtg att tta gtg ~~ggg~~ aaa gat 202
Gln Thr His Lys Arg Pro Lys Leu Ala Val Ile Leu Val Gly Lys Asp
35 40 45

ccc gct agt atc act tat gtc aat atg aag atc aaa gca tgc gaa agg 250
Pro Ala Ser Ile Thr Tyr Val Asn Met Lys Ile Lys Ala Cys Glu Arg
50 55 60 65

gtg ggc atg gat ttt gac tta aaa acc ctc caa gaa aat att act gaa 298
Val Gly Met Asp Phe Asp Leu Lys Thr Leu Gln Glu Asn Ile Thr Glu
70 75 80

gcc aaa ttg cta tcc ttg att aaa gat tac aat acc gat caa aac att 346
Ala Lys Leu Leu Ser Leu Ile Lys Asp Tyr Asn Thr Asp Gln Asn Ile
85 90 95

tca ggc gtt tta gtc cag ctc cct ttg ccc aga cac att gat act aaa Ser Gly Val Leu Val Gln Leu Pro Leu Pro Arg His Ile Asp Thr Lys 100 105 110	394
atg att tta gaa gcc att gac cca aac aaa gat gtg gat ggt ttc cac Met Ile Leu Glu Ala Ile Asp Pro Asn Lys Asp Val Asp Gly Phe His 115 120 125	442
ccc ctt aat atc ggt aag ctc tgc act caa aaa gaa tcg ttt ctg cca Pro Leu Asn Ile Gly Lys Leu Cys Thr Gln Lys Glu Ser Phe Leu Pro 130 135 140 145	490
gcc acc cct atg ggc gtg atg cgg ctt tta gag cat tac cat att gaa Ala Thr Pro Met Gly Val Met Arg Leu Leu Glu His Tyr His Ile Glu 150 155 160	538
atc aag ggt aag gat gtg gcg att att gga gcg agc aat atc att ggc Ile Lys Gly Lys Asp Val Ala Ile Ile Gly Ala Ser Asn Ile Ile Gly 165 170 175	586
aaa cct tta agc atg ctc atg cta aac gct ggg gct agc gtg agc gtg Lys Pro Leu Ser Met Leu Met Leu Asn Ala Gly Ala Ser Val Ser Val 180 185 190	634
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 <213> Helicobacter pylori

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Ala Gln Thr His Lys Arg Pro Lys Leu Ala Val Ile Leu Val Gly Lys
35     40     45
Asp Pro Ala Ser Ile Thr Tyr Val Asn Met Lys Ile Lys Ala Cys Glu
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Arg Val Gly Met Asp Phe Asp Leu Lys Thr Leu Gln Glu Asn Ile Thr
65     70     75     80
Glu Ala Lys Leu Leu Ser Leu Ile Lys Asp Tyr Asn Thr Asp Gln Asn
85     90     95
Ile Ser Gly Val Leu Val Gln Leu Pro Leu Pro Arg His Ile Asp Thr
100    105    110
Lys Met Ile Leu Glu Ala Ile Asp Pro Asn Lys Asp Val Asp Gly Phe
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His Pro Leu Asn Ile Gly Lys Leu Cys Thr Gln Lys Glu Ser Phe Leu
130    135    140
Pro Ala Thr Pro Met Gly Val Met Arg Leu Leu Glu His Tyr His Ile
145    150    155    160
Glu Ile Lys Gly Lys Asp Val Ala Ile Ile Gly Ala Ser Asn Ile Ile
165    170    175
Gly Lys Pro Leu Ser Met Leu Met Leu Asn Ala Gly Ala Ser Val Ser
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Val Cys His Ile Leu Thr Lys Asp Ile Ser Phe Tyr Thr Gln Asn Ala
195    200    205
Asp Ile Val Cys Val Gly Val Gly Lys Pro Asp Leu Ile Lys Ala Ser
210    215    220
Met Leu Lys Lys Gly Ala Val Val Val Asp Ile Gly Ile Asn His Leu
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245    250    255
Val Ala Gly Phe Ile Thr Pro Val Pro Lys Gly Val Gly Pro Met Thr
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<222> (66)...(2099)

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Met Lys Ser Leu Ser Asn Ala Leu Phe Ser Leu Phe Leu Lys Gly
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ttt tat ttc acc ttt ttt atg agc ttg ttg ttt gtg ttt aat cgt atc 158
Phe Tyr Phe Thr Phe Phe Met Ser Leu Leu Phe Val Phe Asn Arg Ile
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gcg tat ttt tct atc gct att atc ctg ttt tta aac att gca aac att Ala Tyr Phe Ser Ile Ala Ile Ile Leu Phe Leu Asn Ile Ala Asn Ile 100 105 110	398
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cct att ttt tct agt ttt tca ctc ttt tta atc ctt agc gtt tta acc Pro Ile Phe Ser Ser Phe Ser Leu Phe Leu Ile Leu Ser Val Leu Thr 145 150 155	542
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gca cgc aat tac aga caa agc cat aac ctt aaa ttc agc gat ttt gct Ala Arg Asn Tyr Arg Gln Ser His Asn Leu Lys Phe Ser Asp Phe Ala 240 245 250 255	830
aaa gaa acg cct tta gaa gtg gcg aaa aat tat ttc cat ctt aaa gag Lys Glu Thr Pro Leu Glu Val Ala Lys Asn Tyr Phe His Leu Lys Glu 260 265 270	878

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Glu	Thr	Pro	Leu 260	Glu	Val	Ala	Lys	Asn 265	Tyr	Phe	His	Leu	Lys 270	Glu	Asn	
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Ser 305	Ser	Trp	His	Phe	Asp 310	Pro	Lys	Phe	Asp	Ala 315	Ile	Gly	Leu	Thr	Ser 320	
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Glu	Ser	Asn 435	Trp	Gly	Val	His	Asp 440	Asn	Ile	Leu	Phe	Asp 445	Tyr	Ile	Leu	
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Leu	Glu	Lys	Ile	Gln 485	Gln	Phe	Val	Glu	Lys 490	Thr	Pro	Lys	Ser	Glu 495	Asn	
Leu	Pro	Asp	Ala 500	Asn	Ser	Leu	Gly	His 505	Ile	Tyr	Trp	Tyr	Asp 510	Lys	Val	

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Phe Ile Ile Thr Gly Asp His Phe Asp Arg Ser Tyr Glu Tyr Ala Lys
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545 550 555 560
Thr Leu Lys Pro Lys Lys Ile Ser Gln Val Gly Ser His Leu Asp Ile
565 570 575
Ala Pro Thr Ile Ile Glu Leu Val Ala Pro Lys Gly Phe Gln Phe Val
580 585 590
Ser Phe Gly Lys Pro Leu Phe Ser Asn Asn Thr Thr Asn Pro Pro Ser
595 600 605
His Pro Asn Tyr Ala Leu Gly Tyr Glu Ala Ile Ala Thr Lys Asp Tyr
610 615 620
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625 630 635 640
Glu Pro Lys Asp Lys Gln Asn Asp Lys Ile Glu Ala Ser Lys Phe Tyr
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35 40 45 50
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Leu Ile Gly Ala Val Ala Leu Leu Val Val Arg Phe Gly Phe Lys Pro
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Lys Tyr Ile Ala Leu Leu Leu Leu Met Ala Ser Ser Gly Leu Tyr Glu
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Ser Phe Tyr His Thr Gly Ser His Ala Leu Glu Asp Val Gly Gln Gly

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Gln	Gly	Phe	Ala	Leu	Ala	Ile	Leu	Gly	Leu	His	Thr	Gln	Phe	Trp	Ala
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Leu	Phe	Val	Phe	Phe	Ser	Val	Val	Val	Leu	Leu	Ala	Val	Leu	Leu	Phe
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Phe	Asn	Glu	Asp	Lys	Ala	Ile	Leu	Thr	Thr	Glu	Asn	Gln	Gly	Leu	Tyr
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Leu	Val	Ser	Asn	Asp	Leu	Lys	Thr	Ile	His	Ser	His	Met	Val	Leu	Asp
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Ser	Tyr	Tyr	Ser	Ala	Thr	Val	Gly	Ser	Phe	Val	Gly	Ala	Asp	Phe	Asn
	290					295					300				
Glu	Asp	Glu	Asn	Ile	Val	Ile	Met	Gly	Asn	Asn	Lys	Thr	Ser	Val	Glu
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060901

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000967

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	1605		1610		1615
Asn Asn Gly	Ser Gly Ser Ser	Ala Arg Arg Glu	Asn Gly Gly Glu	Cys	
	1620		1625		1630
Gly Gly Ala	Ile Ile Lys Ser	Glu Glu Glu Glu	Glu Ser Leu Leu	Leu	
	1635		1640		1645
Ser Ser Thr	Ile Lys Lys Asn	Gln Gln Asp Tyr	Trp Leu Ala Ala	Ala	
	1650		1655		1660
Ala Ile Leu	Arg Arg Met Ser	Tyr Tyr Gln Ser	Ser Ser Leu Ser	Ser Phe	
1665		1670		1675	168
Asn Thr Thr	Thr Gln Gln Gln	Gln Gln Arg Arg	Leu Leu Arg Leu	Leu	
	1685		1690		1695
Asn Ala Lys	Lys His Ala Leu	Leu Val Met Met	Asn Gln Ile Ile	Ile	
	1700		1705		1710
Ile Ile Arg	Gly Gly Glu Leu	Glu Glu Ile Thr	Ser Ser Leu Tyr	Tyr	
	1715		1720		1725
Pro His Leu	Thr Ala Ala Ala	Ala Asn Ala Cys	Cys Leu Asn Gly	Gly	
	1730		1735		1740
Phe Thr Thr	Ala Met Thr Thr	Gln Pro Val Val	Tyr Trp Gly Ser	Ser	
1745		1750		1755	176
Trp Phe Lys	Asp Asp Ser Gly	Ala Ala Trp Cys	Cys Ser Ser Ile	Ile	
	1765		1770		1775
Ile Ile Ile	Tyr Asp Asp Ser	Ser Ser Ser Ala	Ser Leu Leu Lys	Pro	
	1780		1785		1790
Pro Gly Tyr	Ser Ser Pro Leu	Val Val Val Val	Trp Ser Ile Ile	Ile	
	1795		1800		1805
Lys Tyr Tyr	Ser Arg Arg Val	Leu Val Val Asp	Ala Ile Ile Ile	Cys	
	1810		1815		1820
Cys Cys Cys	Cys Gln Phe Phe	Phe Cys Cys Leu	Asn Glu Glu Phe	Cys	
1825		1830		1835	184
Gly Gly Lys	Gly				

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 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (124)...(690)

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gct atg att aat aga gcg acc tta cac aat tat tct gaa att gaa aaa	168
Met Ile Asn Arg Ala Thr Leu His Asn Tyr Ser Glu Ile Glu Lys	
1 5 10 15	
aag aat atc atg ctc agt gat agg gtc gtt gtc att aga agc ggc gat	216
Lys Asn Ile Met Leu Ser Asp Arg Val Val Val Ile Arg Ser Gly Asp	
20 25 30	

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<210> 14
<211> 189
<212> PRT
<213> Helicobacter pylori
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Asn	Ile	Met	Leu	Ser	Asp	Arg	Val	Val	Val	Ile	Arg	Ser	Gly	Asp	Val
			20					25					30		
Ile	Pro	Lys	Ile	Ile	Lys	Pro	Leu	Glu	Ser	Tyr	Arg	Asp	Gly	Ser	Gln
		35					40					45			
His	Lys	Ile	Glu	Arg	Pro	Lys	Val	Cys	Pro	Ile	Cys	Ser	His	Glu	Leu
	50					55					60				
Leu	Cys	Glu	Glu	Ile	Phe	Thr	Tyr	Cys	Gln	Asn	Leu	Asn	Cys	Pro	Ala

106290" E1556860

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Arg	Leu	Lys	Glu	Ser	Leu	Ile	His	Phe	Ala	Ser	Lys	Asp	Ala	Leu	Asn
				85					90					95	
Ile	Gln	Gly	Leu	Gly	Asp	Lys	Val	Ile	Glu	Gln	Leu	Phe	Glu	Glu	Lys
			100					105					110		
Leu	Ile	Phe	Asn	Ala	Leu	Asp	Leu	Tyr	Ala	Leu	Lys	Leu	Glu	Asp	Leu
		115					120					125			
Met	Arg	Leu	Asp	Lys	Phe	Lys	Ile	Lys	Lys	Ala	Gln	Asn	Leu	Leu	Asp
	130					135				140					
Ala	Ile	Leu	Lys	Ser	Lys	Asn	Pro	Pro	Leu	Trp	Arg	Leu	Ile	Asn	Ala
145					150					155				160	
Leu	Gly	Ile	Glu	His	Ile	Gly	Lys	Gly	Ala	Ser	Lys	Thr	Leu	Ala	Lys
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Tyr	Gly	Leu	Asn	Val	Leu	Glu	Lys	Ser	Glu	Xaa	Ser	Phe			
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 <213> Helicobacter pylori

<220>
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Met Arg Pro Gly Val Leu Gln Val Gly Ala Met Tyr Ala Asn Gly Val	
	5 10 15
ggg atc caa acc aac aga tta aaa gcc gct cgc tat tat gaa tgg gtt	152
Gly Ile Gln Thr Asn Arg Leu Lys Ala Ala Arg Tyr Tyr Glu Trp Val	
	20 25 30
gca gcg ggg gcg atg cga ccg ctt gcg cga atc tgg ctc aga tgt atg	200
Ala Ala Gly Ala Met Arg Pro Leu Ala Arg Ile Trp Leu Arg Cys Met	
	35 40 45 50
aaa aca aga aaa atg cgg att caa acg ata aag aaa acg ctt tgc aat	248
Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu Cys Asn	
	55 60 65
tgt atg cgg tgg ctt gtc aag ggg ggg ata tgc tcg cat gca ata att	296
Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala Ile Ile	
	70 75 80
tgg ggt gga tgt ttg cta acg gaa gtg ggg tcc caa aag att att aca	344
Trp Gly Gly Cys Leu Leu Thr Glu Val Gly Ser Gln Lys Ile Ile Thr	
	85 90 95
aag cga taagttatta taaattttca tgcgagaatg ggaatgatat ggggtgttat	400
Lys Arg	
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aat	403

<210> 16
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 <212> PRT
 <213> Helicobacter pylori

<400> 16
 Met Val Met Arg Pro Gly Val Leu Gln Val Gly Ala Met Tyr Ala Asn
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 Gly Val Gly Ile Gln Thr Asn Arg Leu Lys Ala Ala Arg Tyr Tyr Glu
 20 25 30
 Trp Val Ala Ala Gly Ala Met Arg Pro Leu Ala Arg Ile Trp Leu Arg
 35 40 45
 Cys Met Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu
 50 55 60
 Cys Asn Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala
 65 70 75 80
 Ile Ile Trp Gly Gly Cys Leu Leu Thr Glu Val Gly Ser Gln Lys Ile
 85 90 95
 Ile Thr Lys Arg
 100

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 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (51)...(1784)

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 Lys Lys Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His Leu Arg
 5 10 15
 att gaa gtg atc gta gat gat gat aac gtg atc act gat gcg ttt tct 152
 Ile Glu Val Ile Val Asp Asp Asp Asn Val Ile Thr Asp Ala Phe Ser
 20 25 30
 tct tct acg ctt ttt agg ggg cta gaa acc att att aaa ggc aga gat 200
 Ser Ser Thr Leu Phe Arg Gly Leu Glu Thr Ile Ile Lys Gly Arg Asp
 35 40 45 50
 cca cga gat gca ggc ttc atc gct caa agg att tgc ggg gta tgc act 248
 Pro Arg Asp Ala Gly Phe Ile Ala Gln Arg Ile Cys Gly Val Cys Thr
 55 60 65
 tat tcg cat tat aag gcc ggt atc acg gcg gta gaa aac gct cta ggc 296
 Tyr Ser His Tyr Lys Ala Gly Ile Thr Ala Val Glu Asn Ala Leu Gly
 70 75 80
 atc act ccc cca tta aac gcg caa ttg gtg cga tct ttg atg aac atg 344
 Ile Thr Pro Pro Leu Asn Ala Gln Leu Val Arg Ser Leu Met Asn Met
 85 90 95

0065591-062901

gcg ctg ctt ttt cat gac cat gtg gtg cat ttc tat act ttg cat ggg Ala Leu Leu Phe His Asp His Val Val His Phe Tyr Thr Leu His Gly 100 105 110	392
ctt gat tgg tgc gat atc atg agc gct tta aaa gcc gat ccc att caa Leu Asp Trp Cys Asp Ile Met Ser Ala Leu Lys Ala Asp Pro Ile Gln 115 120 125 130	440
gcg gca aaa ctt tct ttc aaa tac agc cct tac cct att aat acc ggt Ala Ala Lys Leu Ser Phe Lys Tyr Ser Pro Tyr Pro Ile Asn Thr Gly 135 140 145	488
gcc ggt gaa tta aaa gcg gtt caa aaa cgc ttg agc gat ttc gct aaa Ala Gly Glu Leu Lys Ala Val Gln Lys Arg Leu Ser Asp Phe Ala Lys 150 155 160	536
agc gga tct ttg ggg cct ttc agt aac ggc tat tac ggg cat aaa act Ser Gly Ser Leu Gly Pro Phe Ser Asn Gly Tyr Tyr Gly His Lys Thr 165 170 175	584
tat cgt tta agt ccg gag caa aat tta atc gtc tta agc cac tac ctc Tyr Arg Leu Ser Pro Glu Gln Asn Leu Ile Val Leu Ser His Tyr Leu 180 185 190	632
aag ctt tta gaa atc caa agg gaa gcg gcg aaa atg acc gct att ttt Lys Leu Leu Glu Ile Gln Arg Glu Ala Ala Lys Met Thr Ala Ile Phe 195 200 205 210	680
ggg gcc aaa cag cct cac cca caa agc cta acg gtg ggg ggt gtt acg Gly Ala Lys Gln Pro His Pro Gln Ser Leu Thr Val Gly Gly Val Thr 215 220 225	728
agt gtt atg gat ata ttg gat ccg acg aga ttg gct gaa tgg aag agc Ser Val Met Asp Ile Leu Asp Pro Thr Arg Leu Ala Glu Trp Lys Ser 230 235 240	776
aag ttt gaa gtg gtg gcc aat ttc atc aac cat gct tac tac cct gat Lys Phe Glu Val Val Ala Asn Phe Ile Asn His Ala Tyr Tyr Pro Asp 245 250 255	824
ttg gtg atg gca ggc gaa atg ttc gct aac gaa caa tcc gtt atc aaa Leu Val Met Ala Gly Glu Met Phe Ala Asn Glu Gln Ser Val Ile Lys 260 265 270	872
ggc tgt ggc tta agg aat ttt atc gct tat gaa gaa gtg ctg ctt ggg Gly Cys Gly Leu Arg Asn Phe Ile Ala Tyr Glu Glu Val Leu Leu Gly 275 280 285 290	920
agg gat aaa tac ctt ttg agt agt ggg gtg gtg ctt gat ggg gat att Arg Asp Lys Tyr Leu Leu Ser Ser Gly Val Val Leu Asp Gly Asp Ile 295 300 305	968
tct aaa tta cac ccc att gat gaa agt ttg att aaa gaa gaa gtt acg Ser Lys Leu His Pro Ile Asp Glu Ser Leu Ile Lys Glu Glu Val Thr 310 315 320	1016
cat tct tgg tat caa tac gaa gac act aaa gaa gtg caa ctc cac cct His Ser Trp Tyr Gln Tyr Glu Asp Thr Lys Glu Val Gln Leu His Pro 325 330 335	1064

tat gac ggg caa acg aac ccg cat tat acc ggt tta aaa gac ggc gag Tyr Asp Gly Gln Thr Asn Pro His Tyr Thr Gly Leu Lys Asp Gly Glu 340 345 350	1112
agc gtg ggg att gaa aat aaa atc atc cct gct aaa gtg ctt gac act Ser Val Gly Ile Glu Asn Lys Ile Ile Pro Ala Lys Val Leu Asp Thr 355 360 365 370	1160
aaa aat aaa tat tct tgg ata aaa tcg ccc aga tac gat agt aag ccc Lys Asn Lys Tyr Ser Trp Ile Lys Ser Pro Arg Tyr Asp Ser Lys Pro 375 380 385	1208
atg gaa gta ggt cct tta agt tcc gta gtg gta ggt tta gcg gcg aaa Met Glu Val Gly Pro Leu Ser Ser Val Val Val Gly Leu Ala Ala Lys 390 395 400	1256
aac cct tat gtt act gaa gtg gct acg aag ttt tta aaa gac act aaa Asn Pro Tyr Val Thr Glu Val Ala Thr Lys Phe Leu Lys Asp Thr Lys 405 410 415	1304
ctg cct tta gag gcg ttg ttt tca acg ctt ggg cga aca gct gca agg Leu Pro Leu Glu Ala Leu Phe Ser Thr Leu Gly Arg Thr Ala Ala Arg 420 425 430	1352
tgt att gaa gct aaa acg atc gct gat aat ggc ctt ttg gcg ttt gat Cys Ile Glu Ala Lys Thr Ile Ala Asp Asn Gly Leu Leu Ala Phe Asp 435 440 445 450	1400
gcg tta gtg gaa aat cta aaa agc gat caa agc act tgt gct cct tat Ala Leu Val Glu Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala Pro Tyr 455 460 465	1448
cac att gat aaa aat caa gaa tat aaa ggg cgc tac att ggt caa gtg His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly Gln Val 470 475 480	1496
cca agg ggc atg cta agc cat tgg gtg cgt att aaa aac ggc gtg gtg Pro Arg Gly Met Leu Ser His Trp Val Arg Ile Lys Asn Gly Val Val 485 490 495	1544
gaa aat tat caa gcg gtg gtg cct tct act tgg aat gca ggg cct aga Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly Pro Arg 500 505 510	1592
gat tct caa aat caa agg ggg gct tat gaa atg agc ttg att ggc act Asp Ser Gln Asn Gln Arg Gly Ala Tyr Glu Met Ser Leu Ile Gly Thr 515 520 525 530	1640
aaa atc gct gat tta acc cag cct tta gaa atc att agg act atc cat Lys Ile Ala Asp Leu Thr Gln Pro Leu Glu Ile Ile Arg Thr Ile His 535 540 545	1688
tct ttt gac cca tgc atc gca tgc tcg gtg cat gtg atg gat ttt aaa Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp Phe Lys 550 555 560	1736
ggg cag tct tta aac gag ttt aaa gta gag cct aat ttc gct aaa ttc Gly Gln Ser Leu Asn Glu Phe Lys Val Glu Pro Asn Phe Ala Lys Phe	1784

565

570

575

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1837

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<211> 578

<212> PRT

<213> Helicobacter pylori

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Leu	Arg	Ile	Glu	Val	Ile	Val	Asp	Asp	Asn	Val	Ile	Thr	Asp	Ala	
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Phe	Ser	Ser	Ser	Thr	Leu	Phe	Arg	Gly	Leu	Glu	Thr	Ile	Ile	Lys	Gly
		35					40					45			
Arg	Asp	Pro	Arg	Asp	Ala	Gly	Phe	Ile	Ala	Gln	Arg	Ile	Cys	Gly	Val
	50					55				60					
Cys	Thr	Tyr	Ser	His	Tyr	Lys	Ala	Gly	Ile	Thr	Ala	Val	Glu	Asn	Ala
65					70					75				80	
Leu	Gly	Ile	Thr	Pro	Leu	Asn	Ala	Gln	Leu	Val	Arg	Ser	Leu	Met	
				85				90					95		
Asn	Met	Ala	Leu	Phe	His	Asp	His	Val	Val	His	Phe	Tyr	Thr	Leu	
			100				105					110			
His	Gly	Leu	Asp	Trp	Cys	Asp	Ile	Met	Ser	Ala	Leu	Lys	Ala	Asp	Pro
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Ile	Gln	Ala	Ala	Lys	Leu	Ser	Phe	Lys	Tyr	Ser	Pro	Tyr	Pro	Ile	Asn
	130					135					140				
Thr	Gly	Ala	Gly	Glu	Leu	Lys	Ala	Val	Gln	Lys	Arg	Leu	Ser	Asp	Phe
145					150					155				160	
Ala	Lys	Ser	Gly	Ser	Leu	Gly	Pro	Phe	Ser	Asn	Gly	Tyr	Tyr	Gly	His
				165					170					175	
Lys	Thr	Tyr	Arg	Leu	Ser	Pro	Glu	Gln	Asn	Leu	Ile	Val	Leu	Ser	His
			180					185					190		
Tyr	Leu	Lys	Leu	Leu	Glu	Ile	Gln	Arg	Glu	Ala	Ala	Lys	Met	Thr	Ala
		195					200					205			
Ile	Phe	Gly	Ala	Lys	Gln	Pro	His	Pro	Gln	Ser	Leu	Thr	Val	Gly	Gly
	210					215					220				
Val	Thr	Ser	Val	Met	Asp	Ile	Leu	Asp	Pro	Thr	Arg	Leu	Ala	Glu	Trp
225					230					235				240	
Lys	Ser	Lys	Phe	Glu	Val	Val	Ala	Asn	Phe	Ile	Asn	His	Ala	Tyr	Tyr
			245						250					255	
Pro	Asp	Leu	Val	Met	Ala	Gly	Glu	Met	Phe	Ala	Asn	Glu	Gln	Ser	Val
			260					265					270		
Ile	Lys	Gly	Cys	Gly	Leu	Arg	Asn	Phe	Ile	Ala	Tyr	Glu	Glu	Val	Leu
		275					280					285			
Leu	Gly	Arg	Asp	Lys	Tyr	Leu	Leu	Ser	Ser	Gly	Val	Val	Leu	Asp	Gly
	290					295					300				
Asp	Ile	Ser	Lys	Leu	His	Pro	Ile	Asp	Glu	Ser	Leu	Ile	Lys	Glu	Glu
305					310					315				320	
Val	Thr	His	Ser	Trp	Tyr	Gln	Tyr	Glu	Asp	Thr	Lys	Glu	Val	Gln	Leu
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His	Pro	Tyr	Asp	Gly	Gln	Thr	Asn	Pro	His	Tyr	Thr	Gly	Leu	Lys	Asp
			340					345					350		
Gly	Glu	Ser	Val	Gly	Ile	Glu	Asn	Lys	Ile	Ile	Pro	Ala	Lys	Val	Leu
		355					360					365			
Asp	Thr	Lys	Asn	Lys	Tyr	Ser	Trp	Ile	Lys	Ser	Pro	Arg	Tyr	Asp	Ser
	370					375					380				
Lys	Pro	Met	Glu	Val	Gly	Pro	Leu	Ser	Ser	Val	Val	Val	Gly	Leu	Ala

T05290" E1656601

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Thr Lys Leu Pro Leu Glu Ala Leu Phe Ser Thr Leu Gly Arg Thr Ala						
		420		425		430
Ala Arg Cys Ile Glu Ala Lys Thr Ile Ala Asp Asn Gly Leu Leu Ala						
		435		440		445
Phe Asp Ala Leu Val Glu Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala						
		450		455		460
Pro Tyr His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly						
		465		470		475
Gln Val Pro Arg Gly Met Leu Ser His Trp Val Arg Ile Lys Asn Gly						
		485		490		495
Val Val Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly						
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Pro Arg Asp Ser Gln Asn Gln Arg Gly Ala Tyr Glu Met Ser Leu Ile						
		515		520		525
Gly Thr Lys Ile Ala Asp Leu Thr Gln Pro Leu Glu Ile Ile Arg Thr						
		530		535		540
Ile His Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp						
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Phe Lys Gly Gln Ser Leu Asn Glu Phe Lys Val Glu Pro Asn Phe Ala						
		565		570		575
Lys Phe						

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<220>
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Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly	
1 5 10	
aat atc ctt ttt ggc gat gaa ggg att ggg gtg cat tta gcc cac tac	160
Asn Ile Leu Phe Gly Asp Glu Gly Ile Gly Val His Leu Ala His Tyr	
15 20 25	
ctc aaa aaa aat ttt tct ttt ttc cct agc gtg gat att ata gat ggg	208
Leu Lys Lys Asn Phe Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly	
30 35 40	
ggg aca atg gcc cag cag ctc att cct tta atc act tcg tat gaa aag	256
Gly Thr Met Ala Gln Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys	
45 50 55	
gtt ttg att ttg gat tgc gtg agc gct gaa ggc gtt gag ata gga tca	304
Val Leu Ile Leu Asp Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser	
60 65 70 75	
gtc tat gct ttt gat ttt aag gac gct cct aaa gaa atc aca tgg gct	352
Val Tyr Ala Phe Asp Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala	

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ggg agc gct cat gaa gtg gaa atg cta cac act tta agg ctc acg gag				400
Gly Ser Ala His Glu Val Glu Met Leu His Thr Leu Arg Leu Thr Glu				
	95	100	105	
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Phe Leu Gly Asp Leu Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe				
	110	115	120	
gtg ata ggg agc gag acc act ttc aag ctt tca agc aaa att tta aac				496
Val Ile Gly Ser Glu Thr Thr Phe Lys Leu Ser Ser Lys Ile Leu Asn				
	125	130	135	
gct tta gaa acc gcc tta aaa gcc ata gaa acc caa ctc aac gca tgg				544
Ala Leu Glu Thr Ala Leu Lys Ala Ile Glu Thr Gln Leu Asn Ala Trp				
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ggg gtt aaa atg caa cgc acc gat cat atc gct tta gaa tgt atc gct				592
Gly Val Lys Met Gln Arg Thr Asp His Ile Ala Leu Glu Cys Ile Ala				
	160	165	170	
gaa ctt tct tat aag ggt ttt tgaattgggtt tttgttttttc tttttaaatg				643
Glu Leu Ser Tyr Lys Gly Phe				
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Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln				
35 40 45				
Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp				
50 55 60				
Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp				
65 70 75 80				
Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu				
85 90 95				
Val Glu Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu				
100 105 110				
Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu				
115 120 125				
Thr Thr Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala				
130 135 140				
Leu Lys Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln				
145 150 155 160				
Arg Thr Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys				
165 170 175				
Gly Phe				

SECRET

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Asn Leu Thr Tyr Tyr Ala Tyr Met Tyr Leu Ile Leu Phe Val Cys Leu															
5 10 15															
ctg cct gtg tta tta atg ggg ctt gtt tgg agg ctt act cgc ccc ccc															152
Leu Pro Val Leu Leu Met Gly Leu Val Trp Arg Leu Thr Arg Pro Pro															
20 25 30															
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Leu Lys Gln Asn Ile Pro Asn Lys Ser Leu Ser Leu Glu Asn Leu Asn															
35 40 45 50															
gaa caa atc aaa aac ctt aaa agc gta cca gct tta gaa aaa ctg aaa															248
Glu Gln Ile Lys Asn Leu Lys Ser Val Pro Ala Leu Glu Lys Leu Lys															
55 60 65															
aac gac ttc aat gag cgt ttt aaa att tgc ccc aaa gat aaa gaa act															296
Asn Asp Phe Asn Glu Arg Phe Lys Ile Cys Pro Lys Asp Lys Glu Thr															
70 75 80															
ctg tgg tta gaa acg atc caa aaa tta gtc gct tca gaa ttt ttt gaa															344
Leu Trp Leu Glu Thr Ile Gln Lys Leu Val Ala Ser Glu Phe Phe Glu															
85 90 95															
tta gaa gac gct att aat ttt ggg caa gaa tta gaa aac gct aac cct															392
Leu Glu Asp Ala Ile Asn Phe Gly Gln Glu Leu Glu Asn Ala Asn Pro															
100 105 110															
aat tac caa caa aaa atc gct aac gct acc ggc tta gcc ctt aag aat															440
Asn Tyr Gln Gln Lys Ile Ala Asn Ala Thr Gly Leu Ala Leu Lys Asn															
115 120 125 130															
aaa aaa gaa aaa gga tagaattgga ttttttagag attgtaggac aagtcctttt															495
Lys Lys Glu Lys Gly															
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tta Leu	aag Lys	gcc Ala	atg Met	acc Thr 135	gct Ala	gca Ala	gaa Glu	gtg Val	cat His 140	ttt Phe	tta Leu	agc Ser	gtt Val	aaa Lys 145	ttc Phe	488
aac Asn	aaa Lys	cct Pro	ttt Phe 150	gaa Glu	ttg Leu	gtg Val	cta Leu	gaa Glu 155	gac Asp	atg Met	ctc Leu	aaa Lys	gcc Ala 160	ggg Gly	gtg Val	536
gat Asp	tcc Ser	atg Met 165	cct Pro	ggc Gly	ggg Gly	ggg Gly	gcg Ala 170	gag Glu	att Ile	ttt Phe	gat Asp 175	gaa Glu	gaa Glu	atc Ile	agg Arg	584
cgt Arg	aaa Lys 180	atc Ile	tgt Cys	aat Asn	ggc Gly	aag Lys 185	gtg Val	gga Gly	tct Ser	tct Ser	cgg Arg 190	tgg Trp	tta Leu	gaa Glu	atc Ile	632
cat His 195	gct Ala	tat Tyr	tgg Trp	cac His 200	aaa Lys	tta Leu	ggc Gly	aaa Lys	atg Met	agt Ser 205	aac Asn	gct Ala	acc Thr	atg Met	ctt Leu 210	680
ttt Phe	ggg Gly	cat His	att Ile	gaa Glu 215	aat Asn	aaa Lys	atc Ile	cat His	cgc Arg 220	atc Ile	gat Asp	cac His	atg Met	cta Leu 225	aga Arg	728
atc Ile	aaa Lys	aaa Lys	atc Ile 230	caa Gln	agc Ser	cct Pro	aaa Lys	aat Asn 235	caa Gln	gta Val	gaa Glu	aac Asn	aaa Lys 240	gaa Glu	ggg Gly	776
ggc Gly	ttt Phe	aac Asn 245	gct Ala	ttt Phe	atc Ile	ccc Pro	ttg Leu 250	ttg Leu	tat Tyr	caa Gln	aaa Lys	gaa Glu 255	aac Asn	aat Asn	tat Tyr	824
ttg Leu	aat Asn 260	gtg Val	gaa Glu	aaa Lys	tcc Ser	ccc Pro 265	agt Ser	gcg Ala	ata Ile	gaa Glu	atc Ile 270	tta Leu	aaa Lys	acc Thr	atc Ile	872
gcc Ala 275	ata Ile	tct Ser	cgc Arg	att Ile 280	ctt Leu	tta Leu	aac Asn	aat Asn	atc Ile	cct Pro 285	cac His	att Ile	aaa Lys	gct Ala	tat Tyr 290	920
tgg Trp	gcg Ala	act Thr	ttg Leu	ggc Gly 295	ttg Leu	aat Asn	ttg Leu	gct Ala	tta Leu 300	gtg Val	gct Ala	caa Gln	gaa Glu	ttt Phe 305	ggc Gly	968
gct Ala	aac Asn	gat Asp	tta Leu 310	gac Asp	ggc Gly	acg Thr	ata Ile	gag Glu 315	ata Ile	gag Glu	agc Ser	att Ile	caa Gln 320	agc Ser	gcg Ala	1016
gca Ala	ggc Gly	gca Ala 325	aag Lys	agc Ser	cgg Arg	cat His	ggc Gly 330	tta Leu	gaa Glu	aaa Lys	gaa Glu	gat Asp 335	ttg Leu	ata Ile	ttt Phe	1064
aaa Lys	atc Ile	aag Lys	gac Asp	gct Ala	ggc Gly	ttt Phe	gtt Val	gcg Ala	gta Val	gaa Glu	agg Arg	gat Asp	agt Ser	ttg Leu	tat Tyr	1112

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1160

1183

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355

360

<210> 25
 <211> 616
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 <213> Helicobacter pylori

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Lys Leu Pro Lys Lys Arg Val Ser Lys Thr Lys Ser Gln Lys Leu Ile		
5	10 15	
cat agc tta acc acc caa aaa aac aga gcc ttt ctc aaa aaa atc agc		152
His Ser Leu Thr Thr Gln Lys Asn Arg Ala Phe Leu Lys Lys Ile Ser		
20	25 30	
gct aat gaa atg ctt tta gaa tta gaa aaa ggg gcg ttt aaa aaa aat		200
Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys Lys Asn		
35	40 45 50	
gaa gct tat ttt att tct gat gaa gaa gat aaa aat tat gtt ttg gtg		248
Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val Leu Val		
55	60 65	
cca gat aac gtg atc tct ctt ttg gca gaa aac gcc aga aag gct ttt		296
Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys Ala Phe		
70	75 80	
gaa gcc agg ctt agg gcg gaa tta gaa agg gat att atc acc caa gcg		344
Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr Gln Ala		
85	90 95	
ccg att gat ttt gaa gac gtg cgc gaa gtt tcc ttg caa cta ttg gaa		392
Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu Leu Glu		
100	105 110	
aat tta cgc caa aaa gat ggg aat ttg cct aat atc aac acc tta aac		440
Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr Leu Asn		
115	120 125 130	
ttt gtc aaa caa atc aaa aaa gaa cac cct aat tta ttc ttt aat ttt		488
Phe Val Lys Gln Ile Lys Lys Glu His Pro Asn Leu Phe Phe Asn Phe		
135	140 145	
gac aac atg ttc aaa caa ccc cct ttt aat gag aat aat ttt gaa aat		536
Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe Glu Asn		
150	155 160	
ttt gac aat agc gat gag gaa aat ttt taatgcaaac cattgatttt		583
Phe Asp Asn Ser Asp Glu Glu Asn Phe		
165	170	

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616

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 <213> Helicobacter pylori

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 20 25 30
 Ile Ser Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys
 35 40 45
 Lys Asn Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val
 50 55 60
 Leu Val Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys
 65 70 75 80
 Ala Phe Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr
 85 90 95
 Gln Ala Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu
 100 105 110
 Leu Glu Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr
 115 120 125
 Leu Asn Phe Val Lys Gln Ile Lys Lys Glu His Pro Asn Leu Phe Phe
 130 135 140
 Asn Phe Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe
 145 150 155 160
 Glu Asn Phe Asp Asn Ser Asp Glu Glu Asn Phe
 165 170

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 Glu Asn Ile Asn Glu Asn Ile Phe Glu Glu Val Gly Asp Ala Cys Val
 5 10 15
 aaa tgc gct aag tgc gtg cca ggc tgc acc ata tac cgc att cat aaa 152
 Lys Cys Ala Lys Cys Val Pro Gly Cys Thr Ile Tyr Arg Ile His Lys
 20 25 30
 gac gag gcg act tcg cct aga ggc ttt tta gat ttg atg cgc tta aac 200
 Asp Glu Ala Thr Ser Pro Arg Gly Phe Leu Asp Leu Met Arg Leu Asn
 35 40 45 50
 gct caa aac aag ctc caa tta gac acg aat tta aaa cac ctt tta gaa 248

005591.06560

acgcctaaaa tctatctggc gagcgtgttt tta

952

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20 25 30
His Lys Asp Glu Ala Thr Ser Pro Arg Gly Phe Leu Asp Leu Met Arg
35 40 45
Leu Asn Ala Gln Asn Lys Leu Gln Leu Asp Thr Asn Leu Lys His Leu
50 55 60
Leu Glu Thr Cys Phe Leu Cys Thr Ala Cys Val Glu Ile Cys Pro Phe
65 70 75 80
His Leu Pro Ile Asp Thr Leu Ile Glu Lys Ala Arg Glu Lys Ile Ala
85 90 95
Gln Lys His Gly Ile Ala Trp Tyr Lys Lys Ser Tyr Phe Ser Leu Leu
100 105 110
Lys Asn Arg Lys Lys Met Asp Arg Val Phe Ser Thr Ala His Phe Leu
115 120 125
Ala Pro Cys Val Phe Lys Gln Val Gly Asp Ser Leu Glu Pro Arg Ala
130 135 140
Val Phe Lys Gly Leu Phe Lys Arg Phe Lys Lys Ser Ala Leu Pro Pro
145 150 155 160
Leu Asn Gln Lys Ser Phe Leu Gln Lys His Ala Glu Met Lys Leu Leu
165 170 175
Glu Asn Pro Ile Gln Lys Val Ala Ile Phe Ile Gly Cys Leu Ser Asn
180 185 190
Tyr His Tyr Gln Gln Val Gly Glu Ser Leu Leu Tyr Ile Leu Glu Lys
195 200 205
Leu Asn Ile Gln Ala Ile Ile Pro Lys Gln Glu Cys Cys Ser Ala Pro
210 215 220
Ala Tyr Phe Thr Gly Asp Lys Asp Thr Thr Leu Phe Leu Val Lys Lys
225 230 235 240
Asn Ile Glu Trp Phe Glu Ser Tyr Leu Asp Lys Val Asp Ala Ile Ile
245 250 255
Val Pro Glu Ala Thr Cys Ala Thr Cys Ser Ser Thr Ile Ile Thr Arg
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Cys Phe Trp Ala Lys Lys Ile Arg Ile Cys Met
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1

57

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aca Thr 20	caa Gln	aat Asn	gcg Ala	cga Arg	tggt Trp 25	ata Ile	gat Asp	caa Gln	aaa Lys	tgc Cys 30	acc Thr	cct Pro	gat Asp	gtg Val	ttg Leu 35	153
tct Ser	ctt Leu	gtt Val	gct Ala 40	gat Asp	tgt Cys	att Ile	tta Leu	gag Glu	ttt Phe 45	acg Thr	caa Gln	tgt Cys	aat Asn	att Ile 50	gga Gly	201
aaa Lys	tca Ser	ttt Phe 55	tct Ser	att Ile	agg Arg	gat Asp	att Ile	tggt Trp 60	gat Asp	agc Ser	cct Pro	tac Tyr	acc Thr 65	aat Asn	gaa Glu	249
aat Asn	gtt Val 70	aaa Lys	atg Met	att Ile	ttt Phe	tct Ser	aaa Lys 75	cct Pro	gat Asp	tta Leu	aat Asn	tct Ser 80	gac Asp	ttt Phe	tcc Ser	297
atg Met 85	cat His	gaa Glu	tac Tyr	gat Asp	aag Lys	ttt Phe 90	ttt Phe	tct Ser	cag Gln	cct Pro	att Ile 95	aaa Lys	tta Leu	tta Leu	gcc Ala	345
tat Tyr 100	agc Ser	ggt Gly	att Ile	tta Leu 105	ttt Phe	gaa Glu	aca Thr	aaa Lys	act Thr	ggc Gly 110	aat Asn	aga Arg	aat Asn	att Ile	tat Tyr 115	393
acc Thr	ata Ile	caa Gln	aac Asn 120	ata Ile	gag Glu	cta Leu	tta Leu	gaa Glu	tat Tyr 125	ctc Leu	atg Met	caa Gln	aga Arg	gaa Glu 130	aca Thr	441
aac Asn	gct Ala	ttg Leu	aaa Lys 135	ttc Phe	ctt Leu	att Ile	tta Leu	tat Tyr 140	att Ile	caa Gln	aag Lys	gta Val	tta Leu 145	atg Met	gat Asp	489
agt Ser	ggg Gly 150	att Ile	tat Tyr	cct Pro	tta Leu	ttt Phe	gac Asp 155	aac Asn	ttt Phe	tta Leu	caa Gln	aaa Lys 160	caa Gln	gac Asp	aca Thr	537
gaa Glu 165	agt Ser	ttt Phe	aag Lys	caa Gln	cta Leu	aaa Lys 170	gat Asp	ggt Gly	ttc Phe	act Thr 175	cat His	ttt Phe	act Thr	atc Ile	aat Asn	585
aac Asn 180	aca Thr	gca Ala	atc Ile	aat Asn	aac Asn 185	gct Ala	acg Thr	gaa Glu	tgt Cys	ttt Phe 190	agg Arg	att Ile	ttt Phe	act Thr 195	aaa Lys	633
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ggg Gly	tat Tyr	ttg Leu 215	tcc Ser	aac Asn	act Thr	ata Ile	att Ile	aca Thr 220	aaa Lys	gat Asp	gag Glu	ctt Leu 225	aat Asn	tat Tyr	aat Asn	729
cgt Arg	atc Ile 230	aat Asn	tggt Trp 235	cga Arg	gat Asp	ata Ile	gga Gly 235	aaa Lys	gat Asp	aaa Lys	aat Asn	acc Thr 240	acc Thr	aga Arg	caa Gln	777

gaa tac gat ctt ata aac tct aaa agg att gct aat tct aac tat ctt 825
 Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser Asn Tyr Leu
 245 250 255

att tca aaa gct aag aaa gtg gtg aaa cga tat aat gat aga ttt aat 873
 Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp Arg Phe Asn
 260 265 270 275

aat tct ctc tct gaa gta aaa caa gaa aaa gaa gag tcg caa gcc aca 921
 Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser Gln Ala Thr
 280 285 290

caa ata cac cat att ttt ccc atc caa gac ttt ccc att att gct aac 969
 Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile Ile Ala Asn
 295 300 305

tat ata gag aat ctt atc gca ctc act cct aat caa cat ttt att tac 1017
 Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His Phe Ile Tyr
 310 315 320

gcc cac cct aat aat caa acc cgc ttg att gat aaa gat ttt caa tat 1065
 Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp Phe Gln Tyr
 325 330 335

atc tgc tta tta gct aaa acg acc aca att ctt aat gac act caa ggc 1113
 Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp Thr Gln Gly
 340 345 350 355

gta tat gat tgg aat gat tat att gtt gtg ttg aat atg ggc ctc aaa 1161
 Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met Gly Leu Lys
 360 365 370

aca act atc ttt tct caa gtc aag aac gaa tgg gaa tta tta aaa gta 1209
 Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu Leu Lys Val
 375 380 385

ata gat gct ttt tat ttt gat ttt aac aag agc aaa gat cca agt tgg 1257
 Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp Pro Ser Trp
 390 395 400

tca tac ttg cta gat aaa aac gat tta aga gct ttc aag cta aaa ttt 1305
 Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys Leu Lys Phe
 405 410 415

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 <213> Helicobacter pylori

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 20 25 30
 Asp Val Leu Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys
 35 40 45

Asn	Ile	Gly	Lys	Ser	Phe	Ser	Ile	Arg	Asp	Ile	Trp	Asp	Ser	Pro	Tyr
50						55					60				
Thr	Asn	Glu	Asn	Val	Lys	Met	Ile	Phe	Ser	Lys	Pro	Asp	Leu	Asn	Ser
65					70					75					80
Asp	Phe	Ser	Met	His	Glu	Tyr	Asp	Lys	Phe	Phe	Ser	Gln	Pro	Ile	Lys
				85					90					95	
Leu	Leu	Ala	Tyr	Ser	Gly	Ile	Leu	Phe	Glu	Thr	Lys	Thr	Gly	Asn	Arg
			100					105					110		
Asn	Ile	Tyr	Thr	Ile	Gln	Asn	Ile	Glu	Leu	Leu	Glu	Tyr	Leu	Met	Gln
		115					120					125			
Arg	Glu	Thr	Asn	Ala	Leu	Lys	Phe	Leu	Ile	Leu	Tyr	Ile	Gln	Lys	Val
		130				135						140			
Leu	Met	Asp	Ser	Gly	Ile	Tyr	Pro	Leu	Phe	Asp	Asn	Phe	Leu	Gln	Lys
145					150					155					160
Gln	Asp	Thr	Glu	Ser	Phe	Lys	Gln	Leu	Lys	Asp	Gly	Phe	Thr	His	Phe
				165					170					175	
Thr	Ile	Asn	Asn	Thr	Ala	Ile	Asn	Asn	Ala	Thr	Glu	Cys	Phe	Arg	Ile
			180					185					190		
Phe	Thr	Lys	Ile	Ile	Asn	Pro	Leu	Ala	Phe	Tyr	Tyr	Gly	Lys	Lys	Gly
		195					200					205			
Thr	Arg	Lys	Gly	Tyr	Leu	Ser	Asn	Thr	Ile	Ile	Thr	Lys	Asp	Glu	Leu
		210					215					220			
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225					230					235					240
Thr	Arg	Gln	Glu	Tyr	Asp	Leu	Ile	Asn	Ser	Lys	Arg	Ile	Ala	Asn	Ser
				245					250					255	
Asn	Tyr	Leu	Ile	Ser	Lys	Ala	Lys	Lys	Val	Val	Lys	Arg	Tyr	Asn	Asp
			260					265					270		
Arg	Phe	Asn	Asn	Ser	Leu	Ser	Glu	Val	Lys	Gln	Glu	Lys	Glu	Glu	Ser
		275					280					285			
Gln	Ala	Thr	Gln	Ile	His	His	Ile	Phe	Pro	Ile	Gln	Asp	Phe	Pro	Ile
		290				295					300				
Ile	Ala	Asn	Tyr	Ile	Glu	Asn	Leu	Ile	Ala	Leu	Thr	Pro	Asn	Gln	His
305					310					315					320
Phe	Ile	Tyr	Ala	His	Pro	Asn	Asn	Gln	Thr	Arg	Leu	Ile	Asp	Lys	Asp
				325					330					335	
Phe	Gln	Tyr	Ile	Cys	Leu	Leu	Ala	Lys	Thr	Thr	Thr	Ile	Leu	Asn	Asp
			340					345					350		
Thr	Gln	Gly	Val	Tyr	Asp	Trp	Asn	Asp	Tyr	Ile	Val	Val	Leu	Asn	Met
			355				360					365			
Gly	Leu	Lys	Thr	Thr	Ile	Phe	Ser	Gln	Val	Lys	Asn	Glu	Trp	Glu	Leu
					375						380				
Leu	Lys	Val	Ile	Asp	Ala	Phe	Tyr	Phe	Asp	Phe	Asn	Lys	Ser	Lys	Asp
385					390					395					400
Pro	Ser	Trp	Ser	Tyr	Leu	Leu	Asp	Lys	Asn	Asp	Leu	Arg	Ala	Phe	Lys
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Phe Ala Met Ile Gly Ser Gly Gly Phe Ile Ala Pro Lys His Leu Gln	
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gcg att aga gat aca ggg cat ttt ttg gat tgc tct ttt gat att cat	154
Ala Ile Arg Asp Thr Gly His Phe Leu Asp Cys Ser Phe Asp Ile His	
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gat agc gtg ggg gtt tta gat gag tat ttc gcg caa tca gag ttt ttt	202
Asp Ser Val Gly Val Leu Asp Glu Tyr Phe Ala Gln Ser Glu Phe Phe	
35 40 45 50	
acg aat att gaa gat ttt gaa aag cat tta gag caa tct aag gat atg	250
Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys Asp Met	
55 60 65	
ggg aaa gaa atc aac tat ttg agt gtt tgc acg cct acg cac acg cat	298
Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His Thr His	
70 75 80	
ttt gat cac atc cgt ttc ggg tta aga aac ggc atg cat gtg att tgt	346
Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val Ile Cys	
85 90 95	
gaa aaa ccc tta gtt tta gac cct ggc gaa ata caa gaa ttg aaa gat	394
Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu Lys Asp	
100 105 110	
tta gag gtg aaa cac caa aaa agg gtg ttt agt ctt tta ccc ttg cgc	442
Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro Leu Arg	
115 120 125 130	
ttg cat tgc gac acg ctg gct ttg aaa gaa aaa att aag agc gaa tta	490
Leu His Cys Asp Thr Leu Ala Leu Lys Glu Lys Ile Lys Ser Glu Leu	
135 140 145	
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Asp Lys Asn Pro Ser Lys Val Phe Asp Ile Thr Leu Thr Tyr Ile Ser	
150 155 160	
gtt caa ggg aaa tgg tat ttt tct tca tgg cga gcg gat gtg aat agg	586
Val Gln Gly Lys Trp Tyr Phe Ser Ser Trp Arg Ala Asp Val Asn Arg	
165 170 175	
agc gga ggg tta gcc act caa atg ggg gtg aat att ttt gac act tta	634
Ser Gly Gly Leu Ala Thr Gln Met Gly Val Asn Ile Phe Asp Thr Leu	
180 185 190	
atc tat ttg ttt gga agc gtt aaa gac aag gtt atc aat aaa gaa gag	682
Ile Tyr Leu Phe Gly Ser Val Lys Asp Lys Val Ile Asn Lys Glu Glu	
195 200 205 210	
cct gat tgc gta ggg gga tac tct ttt tagagcatgc caaaataaga	729
Pro Asp Cys Val Gly Gly Tyr Ser Phe	
215	

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763

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 35 40 45
 Phe Phe Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys
 50 55 60
 Asp Met Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His
 65 70 75 80
 Thr His Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val
 85 90 95
 Ile Cys Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu
 100 105 110
 Lys Asp Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro
 115 120 125
 Leu Arg Leu His Cys Asp Thr Leu Ala Leu Lys Glu Lys Ile Lys Ser
 130 135 140
 Glu Leu Asp Lys Asn Pro Ser Lys Val Phe Asp Ile Thr Leu Thr Tyr
 145 150 155 160
 Ile Ser Val Gln Gly Lys Trp Tyr Phe Ser Ser Trp Arg Ala Asp Val
 165 170 175
 Asn Arg Ser Gly Gly Leu Ala Thr Gln Met Gly Val Asn Ile Phe Asp
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 Leu Leu Arg His Leu Thr Ser Ala Cys Val Phe Leu Ala Ser Lys Cys
 5 10 15
 ttg ccg gac tcc ttt gtc ttg gtc gct ctt tta tcg ttt gtc gtg ttt 152
 Leu Pro Asp Ser Phe Val Leu Val Ala Leu Leu Ser Phe Val Val Phe
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agt tgg ggg aat ggc gct tgg acg ctt tta ggt ttt tct atg caa atg Ser Trp Gly Asn Gly Ala Trp Thr Leu Leu Gly Phe Ser Met Gln Met 55 60 65	248
gcc ctt att ttg gtg ttg ggt cag gct ctg gct aac gct aaa tta gtc Ala Leu Ile Leu Val Leu Gly Gln Ala Leu Ala Asn Ala Lys Leu Val 70 75 80	296
caa aag ctt tta aaa tat cta gcg tct tta cct aaa ggg tat tat acg Gln Lys Leu Leu Lys Tyr Leu Ala Ser Leu Pro Lys Gly Tyr Tyr Thr 85 90 95	344
gct tta tgg ttg gtt act ttt tta tcg tta atc gct aat tgg atc aac Ala Leu Trp Leu Val Thr Phe Leu Ser Leu Ile Ala Asn Trp Ile Asn 100 105 110	392
tgg ggt ttt ggc ttg gtg att agt gcg att ttt gca aaa gag atc gcc Trp Gly Phe Gly Leu Val Ile Ser Ala Ile Phe Ala Lys Glu Ile Ala 115 120 125 130	440
aaa aat gtt aag ggg gtg gat tac agg ctg ctc att gct agc gct tat Lys Asn Val Lys Gly Val Asp Tyr Arg Leu Leu Ile Ala Ser Ala Tyr 135 140 145	488
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Gly Gly Ile Ser Leu Asn Ile Val Asn Thr Ile Phe Leu Phe Leu Gly			
275	280	285	290
att tta ctg cat aaa acc cct tta gct tat gtg aaa gcg atc gat cgt			968
Ile Leu Leu His Lys Thr Pro Leu Ala Tyr Val Lys Ala Ile Asp Arg			
	295	300	305
tcc gct ang agc gtg gct ggg att tta ttg caa ttc cct ttt tac gct			1016
Ser Ala Xaa Ser Val Ala Gly Ile Leu Leu Gln Phe Pro Phe Tyr Ala			
	310	315	320
ggg att atg ggg atg atg gca agc cat agc gtg ggg ggt cat tct tta			1064
Gly Ile Met Gly Met Met Ala Ser His Ser Val Gly Gly His Ser Leu			
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gcg caa atg ctt tct tta gct ttc acg cac atc gct aat gaa aaa act			1112
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	340	345	350
ttc gtg ctc atg act ttt ttg agc gca ggg att gtc aat att ttt att			1160
Phe Val Leu Met Thr Phe Leu Ser Ala Gly Ile Val Asn Ile Phe Ile			
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Pro Ser Gly Gly Gly Gln Trp Ala Ile Gln Ala Pro Ile Met Leu Pro			
	375	380	385
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Ala Gly Gln Ser Leu Gly Val Asp Pro Gly Val Val Ser Met Ala Ile			
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gct tgg gga gat gct tgg acg aat atg ata cag cct ttt tgg gct ttg			1304
Ala Trp Gly Asp Ala Trp Thr Asn Met Ile Gln Pro Phe Trp Ala Leu			
	405	410	415
ccc gct tta gcc att gcg ggt ttg ggc gct aaa gat att atg ggc tat			1352
Pro Ala Leu Ala Ile Ala Gly Leu Gly Ala Lys Asp Ile Met Gly Tyr			
	420	425	430
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Cys Val Leu Thr Leu Ile Phe Val Gly Leu Val Val Cys Gly Val Phe			
	435	440	445
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Tyr Phe Leu Val			
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Trp Met Val Val Ile Gly Ala Leu Ile Cys Met Leu Leu Gly Val Phe	
5 10 15	
atc ttc ttc act agc atg tcg gtt aaa aaa ttt tta agc gct tat ctt	152
Ile Phe Phe Thr Ser Met Ser Val Lys Lys Phe Leu Ser Ala Tyr Leu	
20 25 30	
aac gct tat ttg gat caa cgc ccc cat att aag ggc atg ggg att gca	200
Asn Ala Tyr Leu Asp Gln Arg Pro His Ile Lys Gly Met Gly Ile Ala	
35 40 45 50	
ggc act ccc ttt gaa tgc gaa ggg ttt ttt aaa atc gca tgc gtt tct	248
Gly Thr Pro Phe Glu Cys Glu Gly Phe Phe Lys Ile Ala Cys Val Ser	
55 60 65	
aaa gag ctc agt ttt tta gac tct caa aac tcc cct att gtg aat ttt	296
Lys Glu Leu Ser Phe Leu Asp Ser Gln Asn Ser Pro Ile Val Asn Phe	
70 75 80	
aaa aat ttg agt att aag ctc cgt tct tta gat aaa agc tct ctt act	344
Lys Asn Leu Ser Ile Lys Leu Arg Ser Leu Asp Lys Ser Ser Leu Thr	
85 90 95	
ctt tct gtc cat tct caa atc aaa tcc cct att tta gaa caa gat atg	392
Leu Ser Val His Ser Gln Ile Lys Ser Pro Ile Leu Glu Gln Asp Met	
100 105 110	
cag caa aaa atc agc caa atc ccc cta aaa gac ttg aat gcc tta tta	440
Gln Gln Lys Ile Ser Gln Ile Pro Leu Lys Asp Leu Asn Ala Leu Leu	
115 120 125 130	
gaa aaa atg aaa ccc acg cgc ttg aat tgc tct tta aca ttc aac gct	488
Glu Lys Met Lys Pro Thr Arg Leu Asn Cys Ser Leu Thr Phe Asn Ala	
135 140 145	
cta gat gaa aaa acc tta aac gac aac tta aaa tgc gat ttg act aat	536
Leu Asp Glu Lys Thr Leu Asn Asp Asn Leu Lys Cys Asp Leu Thr Asn	
150 155 160	
gcg gaa aat atc ctt gct tac act ttt ttt caa gag ggt tta atg gag	584
Ala Glu Asn Ile Leu Ala Tyr Thr Phe Phe Gln Glu Gly Leu Met Glu	
165 170 175	
gct caa gaa aat cta tcc ctt aaa aat att ttt aaa acc ttg agt tct	632
Ala Gln Glu Asn Leu Ser Leu Lys Asn Ile Phe Lys Thr Leu Ser Ser	

180	185	190	
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gcg tta gct tct tta gaa aac tat ttt atg gct ttg ttc caa tcc cat Ala Leu Ala Ser Leu Glu Asn Tyr Phe Met Ala Leu Phe Gln Ser His 260 265 270			872
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gcc ttt gtt tct atg gct aaa gac aaa cga tcc caa atc gct ctt aac Ala Phe Val Ser Met Ala Lys Asp Lys Arg Ser Gln Ile Ala Leu Asn 295 300 305			968
gcc caa gct aaa gac aac gcc aag cta act ttt aac gcc ttg tta gaa Ala Gln Ala Lys Asp Asn Ala Lys Leu Thr Phe Asn Ala Leu Leu Glu 310 315 320			1016
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Ile Ala Gly Thr Pro Phe Glu Cys Glu Gly Phe Phe Lys Ile Ala Cys 50 55 60			
Val Ser Lys Glu Leu Ser Phe Leu Asp Ser Gln Asn Ser Pro Ile Val 65 70 75 80			
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Ile Lys Thr His Ser Ser Asn Glu Lys Glu Arg Phe Val Arg Ile Glu																
5 10 15																
gag gac gaa aag aaa gga tta ttt gct gga act gca aat gaa aat tcg																152
Glu Asp Glu Lys Lys Gly Leu Phe Ala Gly Thr Ala Asn Glu Asn Ser																
20 25 30																
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His Gly Leu Ser Leu Met Ala Leu Ile Gly Val Leu Val Phe Gly Gly																
35 40 45 50																
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09895913 052904

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gaa atc gct cat tca agc gtg ttt aaa tcc gcg atg caa gcg tgc gtg Glu Ile Ala His Ser Ser Val Phe Lys Ser Gly Met Gln Ala Cys Val 135 140 145	488
tgc gtg ttg ggc gtg gcg tgg ttg ggc gat act ttt gtg agc aat cat Cys Val Leu Gly Val Ala Trp Leu Gly Asp Thr Phe Val Ser Asn His 150 155 160	536
ata gat gag atc aaa cga tac gct tct ttt ttg atc gca gat tat ccg Ile Asp Glu Ile Lys Arg Tyr Ala Ser Phe Leu Ile Ala Asp Tyr Pro 165 170 175	584
ttt tta tta gcc gta gcg ctc ttt ttg gct tcc atg ctt ttg tat tcg Phe Leu Leu Ala Val Ala Leu Phe Leu Ala Ser Met Leu Leu Tyr Ser 180 185 190	632
caa gcc gcc acc tct aaa gcg ctc atc cca agc gtg atc aca gcc tta Gln Ala Ala Thr Ser Lys Ala Leu Ile Pro Ser Val Ile Thr Ala Leu 195 200 205 210	680
ggc att agc gct aat cat acg gag cat ttg tat att atc gtg gct tcg Gly Ile Ser Ala Asn His Thr Glu His Leu Tyr Ile Ile Val Ala Ser 215 220 225	728
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cta gga gcg atc gct atg gat aac acc gcg acc act aaa atg ggc cgt Leu Gly Ala Ile Ala Met Asp Asn Thr Gly Thr Thr Lys Met Gly Arg 245 250 255	824
tat gtg ttt gat cat gcg ttt ttg atc cct ggg gtt tta gtc gtg tct Tyr Val Phe Asp His Ala Phe Leu Ile Pro Gly Val Leu Val Val Ser 260 265 270	872
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	50					55					60				
Lys	Glu	Thr	Ser	Lys	Asn	Ala	Lys	Leu	Ser	Leu	Trp	Ile	Phe	Ile	Gly
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Gly	Val	Val	Ala	Ile	Val	Phe	Tyr	Ala	Ser	Ala	Ile	Ser	Lys	Asn	Ile
			85						90					95	
Ala	Phe	Val	Ser	Pro	Val	Val	Leu	Gly	Arg	Asp	His	Ala	Ile	Val	Ser
			100					105					110		
Phe	Met	Leu	Ser	Val	Ala	Thr	Leu	Ile	Val	Leu	Phe	Cys	Lys	Ile	Asn
		115					120					125			
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	130					135					140				
Cys	Val	Cys	Val	Leu	Gly	Val	Ala	Trp	Leu	Gly	Asp	Thr	Phe	Val	Ser
	145				150					155					160
Asn	His	Ile	Asp	Glu	Ile	Lys	Arg	Tyr	Ala	Ser	Phe	Leu	Ile	Ala	Asp
			165					170						175	
Tyr	Pro	Phe	Leu	Leu	Ala	Val	Ala	Leu	Phe	Leu	Ala	Ser	Met	Leu	Leu
			180					185					190		
Tyr	Ser	Gln	Ala	Ala	Thr	Ser	Lys	Ala	Leu	Ile	Pro	Ser	Val	Ile	Thr
		195					200					205			
Ala	Leu	Gly	Ile	Ser	Ala	Asn	His	Thr	Glu	His	Leu	Tyr	Ile	Ile	Val
	210					215					220				
Ala	Ser	Phe	Ala	Ser	Val	Ser	Ala	Leu	Phe	Val	Leu	Pro	Thr	Tyr	Pro
	225				230				235						240
Thr	Leu	Leu	Gly	Ala	Ile	Ala	Met	Asp	Asn	Thr	Gly	Thr	Thr	Lys	Met
			245					250						255	
Gly	Arg	Tyr	Val	Phe	Asp	His	Ala	Phe	Leu	Ile	Pro	Gly	Val	Leu	Val
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Glu Asn Ser Ser Ile Trp Ser Asn Pro Ala Phe Val Ala Ile Ile Cys															
5 10 15															
atg tgc gtt ctt agc ctt tta agg ctc aat gtc atg ctt tct atg att															152
Met Cys Val Leu Ser Leu Leu Arg Leu Asn Val Met Leu Ser Met Ile															
20 25 30															
agt gcg act ctc ata gca gga ctt atg gga ggg ctt ggg atc acg gag															200
Ser Ala Thr Leu Ile Ala Gly Leu Met Gly Gly Leu Gly Ile Thr Glu															

35				40				45				50				
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Ser	Phe	Asn	Ala	Met	Ile	Asp	Gly	Met	Lys	Gly	Asn	Leu	Asn	Ile	Ala	
				55					60					65		
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Leu	Ser	Tyr	Ile	Leu	Leu	Gly	Ala	Leu	Ala	Val	Ala	Ile	Ala	Lys	Ser	
			70					75					80			
aat	ctc	att	aaa	gtc	gct	ttg	agt	aaa	tta	ata	ggg	tta	atg	gat	tac	344
Asn	Leu	Ile	Lys	Val	Ala	Leu	Ser	Lys	Leu	Ile	Gly	Leu	Met	Asp	Tyr	
		85					90					95				
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Lys	Arg	Ser	Thr	Phe	Cys	Phe	Leu	Ile	Ala	Phe	Ile	Ala	Cys	Phe	Ser	
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caa	aat	tta	gtg	ccg	gtg	cat	atc	gct	ttt	atc	cct	att	tta	atc	ccc	440
Gln	Asn	Leu	Val	Pro	Val	His	Ile	Ala	Phe	Ile	Pro	Ile	Leu	Ile	Pro	
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cct	ctt	ttg	cat	tta	atg	aac	cgg	cta	gaa	ttg	gat	aga	aga	gcg	gtc	488
Pro	Leu	Leu	His	Leu	Met	Asn	Arg	Leu	Glu	Leu	Asp	Arg	Arg	Ala	Val	
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Ala	Cys	Ala	Leu	Thr	Phe	Gly	Leu	Gln	Ala	Pro	Tyr	Leu	Val	Leu	Pro	
			150					155					160			
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Val	Gly	Phe	Gly	Leu	Ile	Phe	Gln	Thr	Thr	Ile	Leu	Glu	Gln	Leu	Lys	
		165					170					175				
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Ala	Asn	Gly	Val	Ser	Thr	Thr	Ile	Ala	Gln	Ile	Thr	Gly	Val	Met	Trp	
	180					185					190					
ata	gcg	ggg	tta	gcg	atg	gtc	gtt	gga	ctg	ctt	gtt	gct	gta	tta	acg	680
Ile	Ala	Gly	Leu	Ala	Met	Val	Val	Gly	Leu	Leu	Val	Ala	Val	Leu	Thr	
195					200					205					210	
cta	tac	aaa	aaa	ccc	agg	cac	tac	aaa	gag	aaa	tct	ttt	aat	ata	gaa	728
Leu	Tyr	Lys	Lys	Pro	Arg	His	Tyr	Lys	Glu	Lys	Ser	Phe	Asn	Ile	Glu	
				215					220					225		
aat	tac	gcc	tcg	ctt	caa	tta	aac	tac	cat	gac	tac	ttg	act	ttt	ata	776
Asn	Tyr	Ala	Ser	Leu	Gln	Leu	Asn	Tyr	His	Asp	Tyr	Leu	Thr	Phe	Ile	
			230					235					240			
ggg	att	gtc	gta	gcg	ttt	gtg	atc	caa	tta	gcc	acc	gat	tcg	atg	ccc	824
Gly	Ile	Val	Val	Ala	Phe	Val	Ile	Gln								

Lys Phe Lys Glu Thr Asp Ser Leu Met Asp Asp Ser Val Lys Met Met	
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295 300 305	
ttg caa aaa gtg cat gcg ata gag ggc tta gtg aat gcg att aca agc	1016
Leu Gln Lys Val His Ala Ile Glu Gly Leu Val Asn Ala Ile Thr Ser	
310 315 320	
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325 330 335	
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Leu Phe Ile Thr Met Gly Ile Gly Thr Ser Phe Gly Thr Ile Pro Ile	
340 345 350	
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Ile Ala Val Phe Tyr Val Pro Leu Cys Ala Lys Leu Gly Phe Ser Val	
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35 40 45	
Thr Glu Ser Phe Asn Ala Met Ile Asp Gly Met Lys Gly Asn Leu Asn	
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Ile Ala Leu Ser Tyr Ile Leu Leu Gly Ala Leu Ala Val Ala Ile Ala	
65 70 75 80	
Lys Ser Asn Leu Ile Lys Val Ala Leu Ser Lys Leu Ile Gly Leu Met	
85 90 95	
Asp Tyr Lys Arg Ser Thr Phe Cys Phe Leu Ile Ala Phe Ile Ala Cys	
100 105 110	
Phe Ser Gln Asn Leu Val Pro Val His Ile Ala Phe Ile Pro Ile Leu	
115 120 125	
Ile Pro Pro Leu Leu His Leu Met Asn Arg Leu Glu Leu Asp Arg Arg	
130 135 140	
Ala Val Ala Cys Ala Leu Thr Phe Gly Leu Gln Ala Pro Tyr Leu Val	
145 150 155 160	
Leu Pro Val Gly Phe Gly Leu Ile Phe Gln Thr Thr Ile Leu Glu Gln	
165 170 175	
Leu Lys Ala Asn Gly Val Ser Thr Thr Ile Ala Gln Ile Thr Gly Val	
180 185 190	

Gly Lys Ser Asn Lys Lys Val Ser Leu Ala Ser Trp Leu Asn Ser Ser
 180 185 190

<210> 47
 <211> 851
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (49)...(783)

<400> 47
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 Met Asn Phe
 1

tat caa aaa ata tac act cat aaa gtc gtt ttt tct tca ttg ttt ttt 105
 Tyr Gln Lys Ile Tyr Thr His Lys Val Val Phe Ser Ser Leu Phe Phe
 5 10 15

ttg ttg ttt ttg ttc aat gtg gaa act ttg ttg ctt tcg cat ttc agc 153
 Leu Leu Phe Leu Phe Asn Val Glu Thr Leu Leu Leu Ser His Phe Ser
 20 25 30 35

gat gat ttt tcg caa ttg ttt ttt ttg ttt gaa aac cat gtt tat gat 201
 Asp Asp Phe Ser Gln Leu Phe Phe Leu Phe Glu Asn His Val Tyr Asp
 40 45 50

ttc att gtc aaa tta gat tat ttg ggg cta ata ggc gtt tct tta att 249
 Phe Ile Val Lys Leu Asp Tyr Leu Gly Leu Ile Gly Val Ser Leu Ile
 55 60 65

tat ctg ctt gtg ctt att cta aag cct ttc acc ctc acg cgc caa aaa 297
 Tyr Leu Leu Val Leu Ile Leu Lys Pro Phe Thr Leu Thr Arg Gln Lys
 70 75 80

tgc gct tgc gta ggg ata tta tgc ctt tct ttc tac gct tgg aat ttt 345
 Cys Ala Cys Val Gly Ile Leu Cys Leu Ser Phe Tyr Ala Trp Asn Phe
 85 90 95

cct gtt aaa gat tct tta atg gtg ctt tat ctt ttc tat ttt gcg ctg 393
 Pro Val Lys Asp Ser Leu Met Val Leu Tyr Leu Phe Tyr Phe Ala Leu
 100 105 110 115

tta gcg act tta ttg tgg cgt ttt tta ggg gct agc atg aag caa tct 441
 Leu Ala Thr Leu Leu Trp Arg Phe Leu Gly Ala Ser Met Lys Gln Ser
 120 125 130

ttc ttg ccc tct atg aat att tgc atc gtg tgg gtt ttt gct tct tct 489
 Phe Leu Pro Ser Met Asn Ile Cys Ile Val Trp Val Phe Ala Ser Ser
 135 140 145

tta cag agt ttt agg ttt tta agc gtg tct gat tgc gtg gat ttt tcc 537
 Leu Gln Ser Phe Arg Phe Leu Ser Val Ser Asp Cys Val Asp Phe Ser
 150 155 160

ctt ttt aca ctc gcg ctt att tta ttg ata ctg gtt tta atc tat tgc 585

[illegible]

Gly Leu Leu Gly Trp Leu Leu Glu Tyr Val His Asn Thr Leu Arg Arg
 225 230 235 240
 Leu Glu His Gln Ile
 245

<210> 49
 <211> 827
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (95)...(745)

<400> 49
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 ttaagtgcgt tttggtaaaa ttgattatgt gaac atg ctc cct ttt gat gtg ttt 115
 Met Leu Pro Phe Asp Val Phe
 1 5

atc aaa tcc tac ccc acc cct tgt tat ttc aaa caa ttc tta cgg ctt 163
 Ile Lys Ser Tyr Pro Thr Pro Cys Tyr Phe Lys Gln Phe Leu Arg Leu
 10 15 20

aaa aaa acc tac ccc tcc aaa ctc aat gag agt ttt tta ttc agg cgt 211
 Lys Lys Thr Tyr Pro Ser Lys Leu Asn Glu Ser Phe Leu Phe Arg Arg
 25 30 35

att gat gcg ggg ttt att tct tct atc gcc ggc tat cca ttc gct ctt 259
 Ile Asp Ala Gly Phe Ile Ser Ser Ile Ala Gly Tyr Pro Phe Ala Leu
 40 45 50 55

cat tcc cat tct cta ggc att gtc gct tat aag gaa gtt tta agc gtg 307
 His Ser His Ser Leu Gly Ile Val Ala Tyr Lys Glu Val Leu Ser Val
 60 65 70

ctg gtt gtg gat aca aaa aac gct ttt gat aaa gaa agc gct tct tca 355
 Leu Val Val Asp Thr Lys Asn Ala Phe Asp Lys Glu Ser Ala Ser Ser
 75 80 85

aac gcc ctc tct caa gcg cta ggg tta aag ggc gaa gtg tta atc ggc 403
 Asn Ala Leu Ser Gln Ala Leu Gly Leu Lys Gly Glu Val Leu Ile Gly
 90 95 100

aat aaa gca ctg cag ttt tat tat tcc aac cct aaa aaa gat ttt ata 451
 Asn Lys Ala Leu Gln Phe Tyr Tyr Ser Asn Pro Lys Lys Asp Phe Ile
 105 110 115

gat tta gcc gct ctt tgg tat gaa aaa aaa cgc ttg ccg ttt gtt ttt 499
 Asp Leu Ala Ala Leu Trp Tyr Glu Lys Lys Arg Leu Pro Phe Val Phe
 120 125 130 135

ggg cgt ttg tgt tat tac caa aac aag gat ttt tac aag cgc ttg tct 547
 Gly Arg Leu Cys Tyr Tyr Gln Asn Lys Asp Phe Tyr Lys Arg Leu Ser
 140 145 150

tta gct ttc aaa cat caa aaa aca aaa atc cct tac tac atc ctt aaa 595
 Leu Ala Phe Lys His Gln Lys Thr Lys Ile Pro Tyr Tyr Ile Leu Lys
 155 160 165

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-64-

<210> 52
 <211> 196
 <212> PRT
 <213> Helicobacter pylori

<400> 52
 Met Met Gly Tyr Ile Pro Tyr Val Ile Glu Asn Thr Asp Arg Gly Glu
 1 5 10 15
 Arg Ser Tyr Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Val Leu
 20 25 30
 Leu Ser Gly Glu Ile Asn Asp Ser Val Ala Ser Ser Ile Val Ala Gln
 35 40 45
 Leu Leu Phe Leu Glu Ala Glu Asp Pro Glu Lys Asp Ile Gly Leu Tyr
 50 55 60
 Ile Asn Ser Pro Gly Gly Val Ile Thr Ser Gly Leu Ser Ile Tyr Asp
 65 70 75 80
 Thr Met Asn Phe Ile Arg Pro Asp Val Ser Thr Ile Cys Ile Gly Gln
 85 90 95
 Ala Ala Ser Met Gly Ala Phe Leu Leu Ser Cys Gly Ala Lys Gly Lys
 100 105 110
 Arg Phe Ser Leu Pro His Ser Arg Ile Met Ile His Gln Pro Leu Gly
 115 120 125
 Gly Ala Gln Gly Gln Ala Ser Asp Ile Glu Ile Ile Ser Asn Glu Ile
 130 135 140
 Leu Arg Leu Lys Gly Leu Met Asn Ser Ile Leu Ala Gln Asn Ser Gly
 145 150 155 160
 Gln Ser Leu Glu Gln Ile Ala Lys Asp Thr Asp Arg Asp Phe Tyr Met
 165 170 175
 Ser Ala Lys Glu Ala Lys Glu Tyr Gly Leu Ile Asp Lys Val Leu Gln
 180 185 190
 Lys Asn Val Lys
 195

<210> 53
 <211> 904
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)...(852)

<400> 53
 cgc ata aaa aaa gaa cgc ttg aac aaa ctg ctt aaa agg ggg ttt tta 48
 Arg Ile Lys Lys Glu Arg Leu Asn Lys Leu Leu Lys Arg Gly Phe Leu
 1 5 10 15
 gcg ttc ttt ttg agc gtg tat tta agg gct gat gat ttg gtt act tac 96
 Ala Phe Phe Leu Ser Val Tyr Leu Arg Ala Asp Asp Leu Val Thr Tyr
 20 25 30
 acc atc atc aaa gaa aaa gat cta gga tac cag cgg ttt tta gcc aag 144
 Thr Ile Ile Lys Glu Lys Asp Leu Gly Tyr Gln Arg Phe Leu Ala Lys
 35 40 45
 aag tgt tta agg ggt aaa acc cac cct ccg tgt ttt act aag cct aaa 192
 Lys Cys Leu Arg Gly Lys Thr His Pro Pro Cys Phe Thr Lys Pro Lys
 50 55 60

aag cct aaa aga aaa ctt ttt aat ata gac aaa agc tcc cac tat tat	240
Lys Pro Lys Arg Lys Leu Phe Asn Ile Asp Lys Ser Ser His Tyr Tyr	
65 70 75 80	
ggc aca agc gtg gtg caa atg tca tgg cta cag agt agg gaa aaa ttt	288
Gly Thr Ser Val Val Gln Met Ser Trp Leu Gln Ser Arg Glu Lys Phe	
85 90 95	
gaa aac cat tca aaa tac cga gac att cct ttt gct gaa gtc agt ttg	336
Glu Asn His Ser Lys Tyr Arg Asp Ile Pro Phe Ala Glu Val Ser Leu	
100 105 110	
att tat ggc tat aaa caa ttt ttt cct aaa aaa gag cgc tac ggc ttc	384
Ile Tyr Gly Tyr Lys Gln Phe Phe Pro Lys Lys Glu Arg Tyr Gly Phe	
115 120 125	
cgt ttt tat gtc tct ttg gat tac gct tat ggg ttt ttt ctt aaa aat	432
Arg Phe Tyr Val Ser Leu Asp Tyr Ala Tyr Gly Phe Phe Leu Lys Asn	
130 135 140	
aag ggc gtg ttg ggc gat agt ttg agg gag agt tcg caa atc cct aaa	480
Lys Gly Val Leu Gly Asp Ser Leu Arg Glu Ser Ser Gln Ile Pro Lys	
145 150 155 160	
agc tat aga gaa aaa ttg caa aga aaa gag act ttt att aac gct att	528
Ser Tyr Arg Glu Lys Leu Gln Arg Lys Glu Thr Phe Ile Asn Ala Ile	
165 170 175	
ttt tat ggc gcg gga gct gac ttt tta tac aaa cgc gct ttt gga acg	576
Phe Tyr Gly Ala Gly Ala Asp Phe Leu Tyr Lys Arg Ala Phe Gly Thr	
180 185 190	
ctg att tta ggg atg aat ttc gtg gga gaa acc tgg ttt tat gaa aca	624
Leu Ile Leu Gly Met Asn Phe Val Gly Glu Thr Trp Phe Tyr Glu Thr	
195 200 205	
aag att ttt aaa aag tgg gct aaa gat cct ttg agc gtt tat cac cct	672
Lys Ile Phe Lys Lys Trp Ala Lys Asp Pro Leu Ser Val Tyr His Pro	
210 215 220	
tac atg ttt caa gtg atg ttg aat gtg ggg tat cgt tac cgc' ttt tca	720
Tyr Met Phe Gln Val Met Leu Asn Val Gly Tyr Arg Tyr Arg Phe Ser	
225 230 235 240	
agg tat aag aat tgg gcg ata gaa ttg ggt gcg cgc atc cct ttt tta	768
Arg Tyr Lys Asn Trp Ala Ile Glu Leu Gly Ala Arg Ile Pro Phe Leu	
245 250 255	
acc aat gat tat ttt aaa acc cct tta tac acc ctt cat ttc aag cgc	816
Thr Asn Asp Tyr Phe Lys Thr Pro Leu Tyr Thr Leu His Phe Lys Arg	
260 265 270	
aat att tct gtc tat ctc act tca act tat gac ttt tagtttttta	862
Asn Ile Ser Val Tyr Leu Thr Ser Thr Tyr Asp Phe	
275 280	
aatttttgaa aactagaatt aaaaccgctt tttataaact gg	904

<210> 54

<211> 284
 <212> PRT
 <213> Helicobacter pylori

<400> 54

Arg	Ile	Lys	Lys	Glu	Arg	Leu	Asn	Lys	Leu	Leu	Lys	Arg	Gly	Phe	Leu
1				5					10					15	
Ala	Phe	Phe	Leu	Ser	Val	Tyr	Leu	Arg	Ala	Asp	Asp	Leu	Val	Thr	Tyr
			20					25					30		
Thr	Ile	Ile	Lys	Glu	Lys	Asp	Leu	Gly	Tyr	Gln	Arg	Phe	Leu	Ala	Lys
		35					40					45			
Lys	Cys	Leu	Arg	Gly	Lys	Thr	His	Pro	Pro	Cys	Phe	Thr	Lys	Pro	Lys
	50					55					60				
Lys	Pro	Lys	Arg	Lys	Leu	Phe	Asn	Ile	Asp	Lys	Ser	Ser	His	Tyr	Tyr
65					70				75						80
Gly	Thr	Ser	Val	Val	Gln	Met	Ser	Trp	Leu	Gln	Ser	Arg	Glu	Lys	Phe
				85					90					95	
Glu	Asn	His	Ser	Lys	Tyr	Arg	Asp	Ile	Pro	Phe	Ala	Glu	Val	Ser	Leu
			100					105					110		
Ile	Tyr	Gly	Tyr	Lys	Gln	Phe	Phe	Pro	Lys	Lys	Glu	Arg	Tyr	Gly	Phe
		115					120					125			
Arg	Phe	Tyr	Val	Ser	Leu	Asp	Tyr	Ala	Tyr	Gly	Phe	Phe	Leu	Lys	Asn
		130				135					140				
Lys	Gly	Val	Leu	Gly	Asp	Ser	Leu	Arg	Glu	Ser	Ser	Gln	Ile	Pro	Lys
145					150					155					160
Ser	Tyr	Arg	Glu	Lys	Leu	Gln	Arg	Lys	Glu	Thr	Phe	Ile	Asn	Ala	Ile
				165					170					175	
Phe	Tyr	Gly	Ala	Gly	Ala	Asp	Phe	Leu	Tyr	Lys	Arg	Ala	Phe	Gly	Thr
			180					185					190		
Leu	Ile	Leu	Gly	Met	Asn	Phe	Val	Gly	Glu	Thr	Trp	Phe	Tyr	Glu	Thr
		195					200					205			
Lys	Ile	Phe	Lys	Lys	Trp	Ala	Lys	Asp	Pro	Leu	Ser	Val	Tyr	His	Pro
	210					215					220				
Tyr	Met	Phe	Gln	Val	Met	Leu	Asn	Val	Gly	Tyr	Arg	Tyr	Arg	Phe	Ser
225					230					235					240
Arg	Tyr	Lys	Asn	Trp	Ala	Ile	Glu	Leu	Gly	Ala	Arg	Ile	Pro	Phe	Leu
				245					250					255	
Thr	Asn	Asp	Tyr	Phe	Lys	Thr	Pro	Leu	Tyr	Thr	Leu	His	Phe	Lys	Arg
			260					265					270		
Asn	Ile	Ser	Val	Tyr	Leu	Thr	Ser	Thr	Tyr	Asp	Phe				
		275					280								

<210> 55
 <211> 1172
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (75)...(1106)

<400> 55

taatcggttat	taaacatgct	atatttcttt	tttctataaa	actcaatatt	attgaataaa	60
actagggaggt	taga	atg atc tta aaa cga gtt act	gaa gct tta gaa gcg	110		
	Met	Ile Leu Lys Arg Val Thr	Glu Ala Leu Glu Ala			
	1		5		10	
tat aaa aat ggc gaa atg ctc att gtt atg gac gat gaa gac aga gaa	158					
Tyr Lys Asn Gly Glu Met Leu Ile Val Met Asp Asp Glu Asp Arg Glu						

15	20	25	
aat gag ggg gat ttg gtt tta gct ggg att ttt tct acc cct gag aaa Asn Glu Gly Asp Leu Val Leu Ala Gly Ile Phe Ser Thr Pro Glu Lys 30 35 40			206
atc aat ttc atg gcc acg cat gct agg ggg ttg att tgc gtg tct ttg Ile Asn Phe Met Ala Thr His Ala Arg Gly Leu Ile Cys Val Ser Leu 45 50 55 60			254
acc aaa gat tta gcg aaa aaa ttt gaa tta ccc cct atg gtt agc gtg Thr Lys Asp Leu Ala Lys Lys Phe Glu Leu Pro Pro Met Val Ser Val 65 70 75			302
aat gat tct aac cat gag acc gct ttc acg gtt tcc att gac gct aaa Asn Asp Ser Asn His Glu Thr Ala Phe Thr Val Ser Ile Asp Ala Lys 80 85 90			350
gaa gcc aga acc ggg att tct gct ttt gaa agg cat tta acg att gaa Glu Ala Arg Thr Gly Ile Ser Ala Phe Glu Arg His Leu Thr Ile Glu 95 100 105			398
tta ttg tgt aaa gac acc acc aaa ccg agc gat ttt gtg cgc ccg ggg Leu Leu Cys Lys Asp Thr Thr Lys Pro Ser Asp Phe Val Arg Pro Gly 110 115 120			446
cat att ttc cct ttg atc gcc aaa gac ggg ggc gtg tta gcg cgc acg His Ile Phe Pro Leu Ile Ala Lys Asp Gly Gly Val Leu Ala Arg Thr 125 130 135 140			494
ggc cat act gaa gcg agc gtg gat ttg tgc aaa tta gct gga tta aag Gly His Thr Glu Ala Ser Val Asp Leu Cys Lys Leu Ala Gly Leu Lys 145 150 155			542
ccc gtg agc gtg att tgt gaa atc atg aaa gaa gat ggc tct atg gcg Pro Val Ser Val Ile Cys Glu Ile Met Lys Glu Asp Gly Ser Met Ala 160 165 170			590
aga agg ggg gat aaa ttt ttg agc gat ttc gcc ctc aaa cat aac ctt Arg Arg Gly Asp Lys Phe Leu Ser Asp Phe Ala Leu Lys His Asn Leu 175 180 185			638
aaa act ctc tat gtc tct gat ttg att agc tat cgt ttg gaa aat gaa Lys Thr Leu Tyr Val Ser Asp Leu Ile Ser Tyr Arg Leu Glu Asn Glu 190 195 200			686
agt ttg ctg aaa atg ttt tgt caa gaa gaa agg gaa ttt tta aaa cac Ser Leu Leu Lys Met Phe Cys Gln Glu Glu Arg Glu Phe Leu Lys His 205 210 215 220			734
caa acg caa tgc tac act ttt tta gat cac cag caa aaa aac cat tac Gln Thr Gln Cys Tyr Thr Phe Leu Asp His Gln Gln Lys Asn His Tyr 225 230 235			782
gct ttt aag ttt aaa ggc gca aaa acc cat gat tta gcc cct tta gtg Ala Phe Lys Phe Lys Gly Ala Lys Thr His Asp Leu Ala Pro Leu Val 240 245 250			830
cgt ttc cac cct atc aaa gag gat ttt gat ttt tta acg act gat gcg			878

Tyr Thr Phe Leu Asp His Gln Gln Lys Asn His Tyr Ala Phe Lys Phe
 225 230 235 240
 Lys Gly Ala Lys Thr His Asp Leu Ala Pro Leu Val Arg Phe His Pro
 245 250 255
 Ile Lys Glu Asp Phe Asp Phe Leu Thr Thr Asp Ala Phe Glu Val Phe
 260 265 270
 Phe Lys Ala Leu Glu Tyr Leu Lys His Glu Gly Gly Tyr Leu Ile Phe
 275 280 285
 Met Asn Thr His Ser Lys Glu Asn Asn Val Val Lys Asp Phe Gly Ile
 290 295 300
 Gly Ala Leu Val Leu Lys Asn Leu Gly Ile Lys Asp Phe Arg Leu Leu
 305 310 315 320
 Ser Ser Cys Glu Asp Arg Gln Tyr Lys Ala Leu Ser Gly Phe Gly Leu
 325 330 335
 Lys Leu Val Glu Thr Ile Ser Leu
 340

<210> 57
 <211> 394
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(341)

<400> 57
 gattttatcct tgcataaaac aatctcgctt ggcgataaaa aacgctctaa aaa ctt 56
 Lys Leu
 1
 cat ttt aaa gcg ttt cac gca ctt ttc tat cct agc aat aga gac aat 104
 His Phe Lys Ala Phe His Ala Leu Phe Tyr Pro Ser Asn Arg Asp Asn
 5 10 15
 atc tat gcc aat cat tta aaa tta ttg gat aat gaa atc agt gaa aaa 152
 Ile Tyr Ala Asn His Leu Lys Leu Leu Asp Asn Glu Ile Ser Glu Lys
 20 25 30
 gac att ttt aat aaa gcc atc aat caa aaa cga att caa atg gct ctt 200
 Asp Ile Phe Asn Lys Ala Ile Asn Gln Lys Arg Ile Gln Met Ala Leu
 35 40 45 50
 aat ctc atc ttt aag ctt gtt ttt gcc ttt gtt agt aac cac ttc ttc 248
 Asn Leu Ile Phe Lys Leu Val Phe Ala Phe Val Ser Asn His Phe Phe
 55 60 65
 cac gct ttt aga cga cag aat ctc tat aat cgt gtc ttt aat cgc tgt 296
 His Ala Phe Arg Arg Gln Asn Leu Tyr Asn Arg Val Phe Asn Arg Cys
 70 75 80
 gtc ttt aac ctt gac ttc att caa aag ctt ttc att act caa ttc 341
 Val Phe Asn Leu Asp Phe Ile Gln Lys Leu Phe Ile Thr Gln Phe
 85 90 95
 taacgaaata gaagccttaa ggtagcgtct gccattttga gagaccagat tca 394

<210> 58
 <211> 97

<212> PRT
 <213> Helicobacter pylori

<400> 58
 Lys Leu His Phe Lys Ala Phe His Ala Leu Phe Tyr Pro Ser Asn Arg
 1 5 10 15
 Asp Asn Ile Tyr Ala Asn His Leu Lys Leu Leu Asp Asn Glu Ile Ser
 20 25 30
 Glu Lys Asp Ile Phe Asn Lys Ala Ile Asn Gln Lys Arg Ile Gln Met
 35 40 45
 Ala Leu Asn Leu Ile Phe Lys Leu Val Phe Ala Phe Val Ser Asn His
 50 55 60
 Phe Phe His Ala Phe Arg Arg Gln Asn Leu Tyr Asn Arg Val Phe Asn
 65 70 75 80
 Arg Cys Val Phe Asn Leu Asp Phe Ile Gln Lys Leu Phe Ile Thr Gln
 85 90 95
 Phe

<210> 59
 <211> 360
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (82)...(270)

<400> 59
 acttaaaggc ataaaaacct taagcttttt gagtttcaaa agggtttcaa gctttttata 60
 agactttttt tgaatgagta a gga gaa aat att ttg ttc cat aaa ctg atc 111
 Gly Glu Asn Ile Leu Phe His Lys Leu Ile
 1 5 10
 tta aca tgc ttt tta gcg ctt gta gca ata acc att caa gct tgc ggt 159
 Leu Thr Cys Phe Leu Ala Leu Val Ala Ile Thr Ile Gln Ala Cys Gly
 15 20 25
 tat aaa gcc cct cca ttc aat gaa aaa ccc gct aaa aaa act tca aac 207
 Tyr Lys Ala Pro Phe Asn Glu Lys Pro Ala Lys Lys Thr Ser Asn
 30 35 40
 agc tct aat tct tct atg caa acg ccc acc aac agc acc acg cca gaa 255
 Ser Ser Asn Ser Ser Met Gln Thr Pro Thr Asn Ser Thr Thr Pro Glu
 45 50 55
 ttt tta aat cag cct taaaatcact gctcttggtt aagggttttg atttctaggg 310
 Phe Leu Asn Gln Pro
 60
 tttttgtggc taacttttga nsttcgcttt catcatgcgt taccataatg 360

<210> 60
 <211> 63
 <212> PRT
 <213> Helicobacter pylori

<400> 60
 Gly Glu Asn Ile Leu Phe His Lys Leu Ile Leu Thr Cys Phe Leu Ala

1	5	10	15
Leu Val Ala	Ile Thr Ile Gln Ala	Cys Gly Tyr Lys Ala	Pro Pro Phe
	20	25	30
Asn Glu Lys	Pro Ala Lys Lys Thr	Ser Asn Ser Ser	Asn Ser Ser Met
	35	40	45
Gln Thr Pro	Thr Asn Ser Thr Thr	Pro Glu Phe Leu	Asn Gln Pro
	50	55	60

<210> 61
 <211> 445
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(392)

<400> 61
 atttacaaag cgtgttggat accccaaga tgattcgttt ggaaaattga atg cgc 56
 Met Arg
 1

ttt ttg aac aac aaa cat aga gaa aag ggc tta aag gct gaa gaa gaa 104
 Phe Leu Asn Asn Lys His Arg Glu Lys Gly Leu Lys Ala Glu Glu Glu
 5 10 15

gct tgc gga ttt tta aaa tcg tta ggt ttt gaa atg gtg gag agg aac 152
 Ala Cys Gly Phe Leu Lys Ser Leu Gly Phe Glu Met Val Glu Arg Asn
 20 25 30

ttt ttt tca caa ttt ggc gaa att gat att atc gct ttg aaa aaa ggg 200
 Phe Phe Ser Gln Phe Gly Glu Ile Asp Ile Ile Ala Leu Lys Lys Gly
 35 40 45 50

gtt ttg cat ttc att gaa gtc aaa agc ggg gaa aat ttt gat ccc att 248
 Val Leu His Phe Ile Glu Val Lys Ser Gly Glu Asn Phe Asp Pro Ile
 55 60 65

tat gcg atc acg ccg agc aaa tta aaa aag atg att aaa acg atc cgc 296
 Tyr Ala Ile Thr Pro Ser Lys Leu Lys Lys Met Ile Lys Thr Ile Arg
 70 75 80

tgt tat ttg tcc caa aaa gat ccc aat agc gat ttt tgc ata gac gct 344
 Cys Tyr Leu Ser Gln Lys Asp Pro Asn Ser Asp Phe Cys Ile Asp Ala
 85 90 95

ctt att gtg aaa aat ggt aaa ttt gag ctt tta gaa aat atc act ttt 392
 Leu Ile Val Lys Asn Gly Lys Phe Glu Leu Leu Glu Asn Ile Thr Phe
 100 105 110

tagattttta cagaaagtaa atgcgatttc attaacattc ttaagctaata ata 445

<210> 62
 <211> 114
 <212> PRT
 <213> Helicobacter pylori

<400> 62
 Met Arg Phe Leu Asn Asn Lys His Arg Glu Lys Gly Leu Lys Ala Glu

ttt gaa ggc att aga gtg cag ggc ttt ttt aag tat ttc gct cat ttt	496
Phe Glu Gly Ile Arg Val Gln Gly Phe Phe Lys Tyr Phe Ala His Phe	
125 130 135	
gca ggt cct gtg aaa tgg ctc gcc cct ttc atg ttc cct att gag atc	544
Ala Gly Pro Val Lys Trp Leu Ala Pro Phe Met Phe Pro Ile Glu Ile	
140 145 150	
atc tcg cat ttt tct agg atc gtg tct tta tcg ttt cgt ttg ttt ggg	592
Ile Ser His Phe Ser Arg Ile Val Ser Leu Ser Phe Arg Leu Phe Gly	
155 160 165	
aat atc aag ggc gat gac atg ttc ttg ctc atc atg ctt tta tta gtg	640
Asn Ile Lys Gly Asp Met Phe Leu Leu Ile Met Leu Leu Leu Val	
170 175 180 185	
cct tgg gcg gtt cct gta gcg cct ttt atg gtg ttg ttt ttc atg ggg	688
Pro Trp Ala Val Pro Val Ala Pro Phe Met Val Leu Phe Phe Met Gly	
190 195 200	
att tta caa gct ttt gtt ttt atg atc ctc act tat gtg tat ttg gca	736
Ile Leu Gln Ala Phe Val Phe Met Ile Leu Thr Tyr Val Tyr Leu Ala	
205 210 215	
ggg gct gtt tta acc gat gaa ggg cat taagcaataa cattcttgtt	783
Gly Ala Val Leu Thr Asp Glu Gly His	
220 225	
tggctttaat attgtttttt aaaactttgt tttatggtaa agctttta	831
<210> 64	
<211> 226	
<212> PRT	
<213> Helicobacter pylori	
<400> 64	
Met Glu His Arg Val Phe Thr Ile Ala Asn Phe Phe Ser Ser Asn His	
1 5 10 15	
Asp Phe Ile Thr Gly Phe Phe Val Val Leu Thr Ala Val Leu Met Phe	
20 25 30	
Leu Ile Ser Leu Gly Ala Ser Arg Lys Met Gln Met Val Pro Met Gly	
35 40 45	
Leu Gln Asn Val Tyr Glu Ser Ile Ile Ser Ala Ile Leu Ser Val Ala	
50 55 60	
Lys Asp Ile Ile Gly Glu Glu Leu Ala Arg Lys Tyr Phe Pro Leu Ala	
65 70 75 80	
Gly Thr Ile Ala Leu Tyr Val Phe Phe Ser Asn Met Ile Gly Ile Ile	
85 90 95	
Pro Gly Phe Glu Ser Pro Thr Ala Ser Trp Ser Phe Thr Leu Val Leu	
100 105 110	
Ala Leu Ile Val Phe Phe Tyr Tyr His Phe Glu Gly Ile Arg Val Gln	
115 120 125	
Gly Phe Phe Lys Tyr Phe Ala His Phe Ala Gly Pro Val Lys Trp Leu	
130 135 140	
Ala Pro Phe Met Phe Pro Ile Glu Ile Ile Ser His Phe Ser Arg Ile	
145 150 155 160	
Val Ser Leu Ser Phe Arg Leu Phe Gly Asn Ile Lys Gly Asp Asp Met	
165 170 175	
Phe Leu Leu Ile Met Leu Leu Leu Val Pro Trp Ala Val Pro Val Ala	

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<220>  
<221> CDS  
<222> (51) ... (734)
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-75-

Ser	Pro	Ile	Thr	Gln	Ser	Asn	Leu	Lys	Arg	Leu	Lys	Asp	Ser	Asn	His		
			150					155					160				
att	att	tta	gac	acc	aaa	aac	gcc	ctt	tta	gca	tgc	gac	act	aaa	ggc	584	
Ile	Ile	Leu	Asp	Thr	Lys	Asn	Ala	Leu	Leu	Ala	Cys	Asp	Thr	Lys	Gly		
		165					170					175					
gat	ggg	gcg	atg	gct	gag	cct	tta	gaa	atc	ctt	ttt	aaa	gcc	gct	caa	632	
Asp	Gly	Ala	Met	Ala	Glu	Pro	Leu	Glu	Ile	Leu	Phe	Lys	Ala	Ala	Gln		
	180					185					190						
acg	ctc	cta	aaa	gac	gct	tat	ttt	gaa	aac	aga	gaa	gtc	ata	gtc	atg	680	
Thr	Leu	Leu	Lys	Asp	Ala	Tyr	Phe	Glu	Asn	Arg	Glu	Val	Ile	Val	Met		
195				200					205						210		
ggc	ggc	gcg	agt	ata	gaa	aag	att	gac	agc	gtt	cga	acg	att	agc	aat	728	
Gly	Gly	Ala	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Arg	Thr	Ile	Ser	Asn		
			215					220					225				
act	ttc	tagcgggatt	caagcgagcg	ctttagcttt	ggcggttatat	tttaagggag										784	
Thr	Phe																

cca 787

<210> 66
 <211> 228
 <212> PRT
 <213> Helicobacter pylori

<400> 66

Met	Asn	Phe	Leu	Glu	Asp	Leu	Phe	Tyr	Pro	Leu	Arg	Leu	Leu	Glu	Asn		
1			5						10					15			
Lys	Arg	Val	Leu	Leu	Leu	Val	Ser	Gly	Ser	Ile	Ala	Ala	Tyr	Lys	Ser		
		20						25					30				
Leu	Glu	Leu	Val	Arg	Leu	Leu	Phe	Lys	Ser	Gly	Ala	Ser	Ile	Gln	Val		
	35					40					45						
Val	Met	Ser	Lys	Gly	Ala	Lys	Lys	Phe	Ile	Lys	Pro	Leu	Ser	Phe	Glu		
	50					55					60						
Ala	Leu	Ser	His	His	Lys	Val	Leu	His	Asp	Arg	Asn	Glu	Lys	Trp	Tyr		
65				70					75					80			
Tyr	Asn	His	Gln	Asn	Ala	Leu	His	His	Asn	His	Ile	Ala	Cys	Ala	Ala		
			85					90					95				
Asn	Ala	Asp	Leu	Leu	Ile	Phe	Ala	Pro	Leu	Ser	Thr	Asn	Ser	Leu	Ser		
		100					105					110					
Lys	Ile	Ala	His	Ala	Leu	Ala	Asp	Asn	Ile	Val	Ser	Ala	Thr	Phe	Leu		
	115					120						125					
Ala	Cys	Ala	Ser	Pro	Lys	Ile	Leu	Ala	Pro	Ser	Met	Asn	Thr	Asn	Met		
	130				135					140							
Leu	Asn	Ser	Pro	Ile	Thr	Gln	Ser	Asn	Leu	Lys	Arg	Leu	Lys	Asp	Ser		
145				150					155					160			
Asn	His	Ile	Ile	Leu	Asp	Thr	Lys	Asn	Ala	Leu	Leu	Ala	Cys	Asp	Thr		
			165					170					175				
Lys	Gly	Asp	Gly	Ala	Met	Ala	Glu	Pro	Leu	Glu	Ile	Leu	Phe	Lys	Ala		
		180				185						190					
Ala	Gln	Thr	Leu	Leu	Lys	Asp	Ala	Tyr	Phe	Glu	Asn	Arg	Glu	Val	Ile		
	195					200					205						
Val	Met	Gly	Gly	Ala	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Arg	Thr	Ile		
	210					215				220							

Ser Asn Thr Phe
225

<210> 67
<211> 1078
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (71)...(1009)

<400> 67
tcccaagccc taaaggcgct tcaatcattg attttaaaagg cagttatgaa gagtatttgg 60
cgagcaaaaa atg aaa ccg caa gac att gaa atc gtt caa agc gtt tta 109
Met Lys Pro Gln Asp Ile Glu Ile Val Gln Ser Val Leu
1 5 10
gag att aca gga ccg att aag cct act gaa gtg tat gat aaa gcc aaa 157
Glu Ile Thr Gly Pro Ile Lys Pro Thr Glu Val Tyr Asp Lys Ala Lys
15 20 25
gag ctt ttt gaa aaa ggt gag att aca aac atg ttt gat tgt ggg ggc 205
Glu Leu Phe Glu Lys Gly Glu Ile Thr Asn Met Phe Asp Cys Gly Gly
30 35 40 45
aaa acc ccg cac cag agc gtt agt tct tat att tat aca gcc tta aac 253
Lys Thr Pro His Gln Ser Val Ser Ser Tyr Ile Tyr Thr Ala Leu Asn
50 55 60
aag ggc gaa gaa ctg cct ttt aaa aaa gtg caa gaa aac cca acc tta 301
Lys Gly Glu Glu Leu Pro Phe Lys Lys Val Gln Glu Asn Pro Thr Leu
65 70 75
atc gct tta aaa gac gcg gct aaa gag cta ggt tta gac gct caa aaa 349
Ile Ala Leu Lys Asp Ala Ala Lys Glu Leu Gly Leu Asp Ala Gln Lys
80 85 90
ata agc gct cca agc tct aaa atc gcg cat gaa agg gat ttg cac ccc 397
Ile Ser Ala Pro Ser Ser Lys Ile Ala His Glu Arg Asp Leu His Pro
95 100 105
ttt tta acc tac atg gct att aat aac gaa aat ttg aaa tgc tac acg 445
Phe Leu Thr Tyr Met Ala Ile Asn Asn Glu Asn Leu Lys Cys Tyr Thr
110 115 120 125
aaa acc att ttt cat gaa gag agt tca aaa tca ata aaa ggc atg gac 493
Lys Thr Ile Phe His Glu Glu Ser Ser Lys Ser Ile Lys Gly Met Asp
130 135 140
agg tgg ctt tat ccg gac atg gtg ggg gtt agg ttt ttg cac gct gaa 541
Arg Trp Leu Tyr Pro Asp Met Val Gly Val Arg Phe Leu His Ala Glu
145 150 155
tta tct aat gaa aat tta atc gct ttt tct aag aaa ttt gac act tta 589
Leu Ser Asn Glu Asn Leu Ile Ala Phe Ser Lys Lys Phe Asp Thr Leu
160 165 170
ccc att aaa ctg gtg agc ttt gaa ttg aaa aaa gaa atc agc gtg cat 637

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Phe His Glu Glu Ser Ser Lys Ser Ile Lys Gly Met Asp Arg Trp Leu
 130 135 140
 Tyr Pro Asp Met Val Gly Val Arg Phe Leu His Ala Glu Leu Ser Asn
 145 150 155 160
 Glu Asn Leu Ile Ala Phe Ser Lys Lys Phe Asp Thr Leu Pro Ile Lys
 165 170 175
 Leu Val Ser Phe Glu Leu Lys Lys Glu Ile Ser Val His Asn Cys Arg
 180 185 190
 Glu Cys Tyr Phe Gln Ala Ile Ser Asn Ser Ser Trp Ala Asn Glu Gly
 195 200 205
 Tyr Leu Val Gly Arg His Ile Asp Thr His Asn Pro Gln Leu Met Asp
 210 215 220
 Leu Leu Lys Arg Leu His Ala Ser Phe Gly Ile Gly Val Ile Asp Leu
 225 230 235 240
 Arg Thr Asn Glu Asp Lys Ser Ala Ile Leu Leu Asn Ala Lys Tyr Lys
 245 250 255
 Glu Lys Ile Asp Tyr Thr Val Ala Ser Glu Leu Ser Ala Lys Asn Glu
 260 265 270
 Lys Phe Ser Gly Phe Leu Lys Ser Val Val Asp Tyr Asp Pro Asn His
 275 280 285
 Pro Gln Arg Tyr Lys Asp Glu Phe Asp Glu Val Lys Lys Lys Glu Glu
 290 295 300
 Leu Tyr Pro Asn Pro Ser Leu Ser Phe
 305 310

<210> 69
 <211> 444
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (112)...(375)

<400> 69

aactcgccctt aggcgcgatg gcgtttaagg aagtcaagct ttttgaattt ggcgagcaat 60
 taagggattt tgtactatat tgaagatgtg atccaagcga gcgtgaaaagc g atg aag 117
 Met Lys
 1
 gct caa aaa agc ggg gtt tat aat gtg ggt tat tcc caa gcc aga agt 165
 Ala Gln Lys Ser Gly Val Tyr Asn Val Gly Tyr Ser Gln Ala Arg Ser
 5 10 15
 tat aat gaa atc gtt agc att tta aaa gag cat tta ggg gat ttt aaa 213
 Tyr Asn Glu Ile Val Ser Ile Leu Lys Glu His Leu Gly Asp Phe Lys
 20 25 30
 gtg agt tat atc aaa aac cct tat gct ttc ttc caa aag cac acc caa 261
 Val Ser Tyr Ile Lys Asn Pro Tyr Ala Phe Phe Gln Lys His Thr Gln
 35 40 45 50
 gca cac att gag cct gct att ttg gat ttg gat tac acc cct tta tac 309
 Ala His Ile Glu Pro Ala Ile Leu Asp Leu Asp Tyr Thr Pro Leu Tyr
 55 60 65
 gat ttg gaa agc ggc att aaa gat tat ttg ccc cat atc cat gcg att 357
 Asp Leu Glu Ser Gly Ile Lys Asp Tyr Leu Pro His Ile His Ala Ile
 70 75 80

ttt aaa gga cag tgc gca tgaaaaaaat cttagtcata ggcgatctga 405
Phe Lys Gly Gln Cys Ala
85

tcgctgatta ttattttgtgg gggaagagcg aacggcttt 444

<210> 70
<211> 88
<212> PRT
<213> Helicobacter pylori

<400> 70
Met Lys Ala Gln Lys Ser Gly Val Tyr Asn Val Gly Tyr Ser Gln Ala
1 5 10 15
Arg Ser Tyr Asn Glu Ile Val Ser Ile Leu Lys Glu His Leu Gly Asp
20 25 30
Phe Lys Val Ser Tyr Ile Lys Asn Pro Tyr Ala Phe Phe Gln Lys His
35 40 45
Thr Gln Ala His Ile Glu Pro Ala Ile Leu Asp Leu Asp Tyr Thr Pro
50 55 60
Leu Tyr Asp Leu Glu Ser Gly Ile Lys Asp Tyr Leu Pro His Ile His
65 70 75 80
Ala Ile Phe Lys Gly Gln Cys Ala
85

<210> 71
<211> 822
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (153)...(728)

<400> 71
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atTTTTcaat cttttgtcta aaatttttaat ggggggtttt gggctttata tcctttatat 120
ggggatcatg ctcattaacc acaaaatgcc tc atg cca tgc atc atc aaa aca 173
Met Pro Cys Ile Ile Lys Thr
1 5

aca cca ctc agc atg atc ata aag gag tgc att cgc atg aac act aac 221
Thr Pro Leu Ser Met Ile Ile Lys Glu Cys Ile Arg Met Asn Thr Asn
10 15 20

aaa gcc ctt ttt ttg gac aga gac ggc att atc aat att gat aaa ggc 269
Lys Ala Leu Phe Leu Asp Arg Asp Gly Ile Ile Asn Ile Asp Lys Gly
25 30 35

tat gtg agt caa aaa gaa gat ttt gag ttt caa aaa ggg att ttt gaa 317
Tyr Val Ser Gln Lys Glu Asp Phe Glu Phe Gln Lys Gly Ile Phe Glu
40 45 50 55

ttg cta aag cat gcg aaa tct tta ggc tac aaa ctg ctt tta atc acc 365
Leu Leu Lys His Ala Lys Ser Leu Gly Tyr Lys Leu Leu Leu Ile Thr
60 65 70

aac caa tct ggg atc aac cga ggc tat tac acc ctt aaa gat ttt gaa 413

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Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr	Tyr	Thr	Leu	Lys	Asp	Phe	Glu		
			75					80					85				
caa	ctc	acc	caa	tac	ctc	caa	gaa	agc	ttg	ttc	aaa	gaa	tta	ggg	ttt	461	
Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser	Leu	Phe	Lys	Glu	Leu	Gly	Phe		
			90				95					100					
aat	ctg	gat	ggc	atc	tat	ttt	tgc	agg	cac	gcc	cca	gaa	gaa	aat	tgc	509	
Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg	His	Ala	Pro	Glu	Glu	Asn	Cys		
			105			110					115						
gct	tgc	agg	aag	cca	aag	cct	tct	ttg	att	ttg	caa	gct	gct	aaa	gag	557	
Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu	Ile	Leu	Gln	Ala	Ala	Lys	Glu		
					125					130					135		
cat	caa	att	tgc	ttg	gag	caa	tct	ttt	atg	ata	ggc	gat	aaa	gag	agc	605	
His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe	Met	Ile	Gly	Asp	Lys	Glu	Ser		
				140					145					150			
gac	atg	tta	gcc	ggc	ttg	aac	gct	aaa	gtt	aaa	aat	aac	ctt	ttg	ctc	653	
Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys	Val	Lys	Asn	Asn	Leu	Leu	Leu		
			155					160					165				
att	caa	aac	cct	tta	aaa	act	cct	cat	tct	tgg	ata	caa	tgt	aaa	gat	701	
Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His	Ser	Trp	Ile	Gln	Cys	Lys	Asp		
			170				175					180					
ttt	aaa	gag	atg	ata	gat	cta	atc	aaa	taaggacaag	aatgcgttat						748	
Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys									
			185			190											
attgatgatg	aattagaaaa	tcaaacgatt	ttaatcacccg	gtggggctgg	ctttgtaggc	808											
agtaatctag	cctt					822											

<210> 72
 <211> 192
 <212> PRT
 <213> Helicobacter pylori

<400> 72

Met	Pro	Cys	Ile	Ile	Lys	Thr	Thr	Pro	Leu	Ser	Met	Ile	Ile	Lys	Glu
1				5					10					15	
Cys	Ile	Arg	Met	Asn	Thr	Asn	Lys	Ala	Leu	Phe	Leu	Asp	Arg	Asp	Gly
			20					25					30		
Ile	Ile	Asn	Ile	Asp	Lys	Gly	Tyr	Val	Ser	Gln	Lys	Glu	Asp	Phe	Glu
		35				40						45			
Phe	Gln	Lys	Gly	Ile	Phe	Glu	Leu	Leu	Lys	His	Ala	Lys	Ser	Leu	Gly
	50				55					60					
Tyr	Lys	Leu	Leu	Leu	Ile	Thr	Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr
65					70					75				80	
Tyr	Thr	Leu	Lys	Asp	Phe	Glu	Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser
			85					90						95	
Leu	Phe	Lys	Glu	Leu	Gly	Phe	Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg
			100					105					110		
His	Ala	Pro	Glu	Glu	Asn	Cys	Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu
		115					120					125			
Ile	Leu	Gln	Ala	Ala	Lys	Glu	His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe
	130					135					140				
Met	Ile	Gly	Asp	Lys	Glu	Ser	Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys

145		150		155		160									
Val	Lys	Asn	Asn	Leu	Leu	Leu	Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His
			165					170						175	
Ser	Trp	Ile	Gln	Cys	Lys	Asp	Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys
			180					185					190		

<210> 73
 <211> 831
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (88)...(756)

<400> 73
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 ctttagaaat gaataagaag taggcct atg cca gct agg caa tct ttt aca gat 114
 Met Pro Ala Arg Gln Ser Phe Thr Asp
 1 5

ttg aaa aac ctg gtt ttg tgc gat ata ggc aac acg cgt atc cat ttt 162
 Leu Lys Asn Leu Val Leu Cys Asp Ile Gly Asn Thr Arg Ile His Phe
 10 15 20 25

gca caa aac tat cag ctc ttt tca agc gct aaa gaa gat tta aag cgt 210
 Ala Gln Asn Tyr Gln Leu Phe Ser Ser Ala Lys Glu Asp Leu Lys Arg
 30 35 40

ttg ggt att caa aag gaa att ttt tac att agc gtg aat gaa gaa aat 258
 Leu Gly Ile Gln Lys Glu Ile Phe Tyr Ile Ser Val Asn Glu Glu Asn
 45 50 55

gaa aaa gcc ctt ttg aat tgt tac cct aac gct aaa aat att gca ggg 306
 Glu Lys Ala Leu Leu Asn Cys Tyr Pro Asn Ala Lys Asn Ile Ala Gly
 60 65 70

ttt ttt cat tta gaa acc gac tat gta ggg ctt ggg ata gac cgg caa 354
 Phe Phe His Leu Glu Thr Asp Tyr Val Gly Leu Gly Ile Asp Arg Gln
 75 80 85

atg gcg tgt ctg gcg gta aat aat ggc gtg gtg gtg gat gcc ggg agt 402
 Met Ala Cys Leu Ala Val Asn Asn Gly Val Val Val Asp Ala Gly Ser
 90 95 100 105

gcg att acg ata gat tta atc aaa gag ggc aag cat tta gga ggg tgt 450
 Ala Ile Thr Ile Asp Leu Ile Lys Glu Gly Lys His Leu Gly Gly Cys
 110 115 120

att tta ccc ggt tta gcc caa tat att cat gcg tat aaa aaa agc gct 498
 Ile Leu Pro Gly Leu Ala Gln Tyr Ile His Ala Tyr Lys Lys Ser Ala
 125 130 135

aaa att tta gag caa cct ttc aag gcc tta gat tct tta gaa gtt tta 546
 Lys Ile Leu Glu Gln Pro Phe Lys Ala Leu Asp Ser Leu Glu Val Leu
 140 145 150

cct aaa agc act aga gac gct gtg aat tac ggc atg gtt ttg agc gtc 594
 Pro Lys Ser Thr Arg Asp Ala Val Asn Tyr Gly Met Val Leu Ser Val

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155

160

165

att gct tgt atc cag cat tta gcc aaa aat caa aaa atc tat ctt tgt 642
 Ile Ala Cys Ile Gln His Leu Ala Lys Asn Gln Lys Ile Tyr Leu Cys
 170 175 180 185

ggg ggc gat gcg aag tat ttg agc gcg ttt tta ccc cat tct gtt tgc 690
 Gly Gly Asp Ala Lys Tyr Leu Ser Ala Phe Leu Pro His Ser Val Cys
 190 195 200

aag gag cgt ttg gtt ttt gac ggg atg gaa atc gct ctt aaa aaa gca 738
 Lys Glu Arg Leu Val Phe Asp Gly Met Glu Ile Ala Leu Lys Lys Ala
 205 210 215

ggg ata cta gaa tgc aaa tgatgcacaa tttgagtttt ttgggcatgt 786
 Gly Ile Leu Glu Cys Lys
 220

ttttagccgc tttgagcatg tcttttagggc attgtgtggg catgt 831

<210> 74

<211> 223

<212> PRT

<213> Helicobacter pylori

<400> 74

Met Pro Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys
 1 5 10 15
 Asp Ile Gly Asn Thr Arg Ile His Phe Ala Gln Asn Tyr Gln Leu Phe
 20 25 30
 Ser Ser Ala Lys Glu Asp Leu Lys Arg Leu Gly Ile Gln Lys Glu Ile
 35 40 45
 Phe Tyr Ile Ser Val Asn Glu Glu Asn Glu Lys Ala Leu Leu Asn Cys
 50 55 60
 Tyr Pro Asn Ala Lys Asn Ile Ala Gly Phe Phe His Leu Glu Thr Asp
 65 70 75 80
 Tyr Val Gly Leu Gly Ile Asp Arg Gln Met Ala Cys Leu Ala Val Asn
 85 90 95
 Asn Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile Asp Leu Ile
 100 105 110
 Lys Glu Gly Lys His Leu Gly Gly Cys Ile Leu Pro Gly Leu Ala Gln
 115 120 125
 Tyr Ile His Ala Tyr Lys Lys Ser Ala Lys Ile Leu Glu Gln Pro Phe
 130 135 140
 Lys Ala Leu Asp Ser Leu Glu Val Leu Pro Lys Ser Thr Arg Asp Ala
 145 150 155 160
 Val Asn Tyr Gly Met Val Leu Ser Val Ile Ala Cys Ile Gln His Leu
 165 170 175
 Ala Lys Asn Gln Lys Ile Tyr Leu Cys Gly Gly Asp Ala Lys Tyr Leu
 180 185 190
 Ser Ala Phe Leu Pro His Ser Val Cys Lys Glu Arg Leu Val Phe Asp
 195 200 205
 Gly Met Glu Ile Ala Leu Lys Lys Ala Gly Ile Leu Glu Cys Lys
 210 215 220

<210> 75

<211> 1780

<212> DNA

<213> Helicobacter pylori

<220>
 <221> CDS
 <222> (195)...(1709)

<400> 75

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ttcattctta	aaaaaaggat	tttttaagga	aattgaatct	tgtagtctt	tgtataacaa	120
attatgtgat	aatcaccaca	agtaatcggc	ttagtgtcat	attacgaaga	tttaagatca	180
taaaaggaaa	aaag atg gtt	aat aaa gat	gtg aaa caa	acc act gct	ttt	230
	Met Val Asn	Lys Asp Val	Lys Gln Thr	Thr Ala Phe		
	1	5	10			
ggc gct ccc	gtt tgg gat	gac aac aat	gtg att acg	gcc ggc cct	aga	278
Gly Ala Pro	Val Trp Asp	Asp Asn Asn	Val Ile Thr	Ala Gly Pro	Arg	
	15	20	25			
ggt cct gtt	tta tta caa	agc act tgg	ttt ttg gaa	aag tta gcg	gcg	326
Gly Pro Val	Leu Leu Gln	Ser Thr Trp	Phe Leu Glu	Lys Leu Ala	Ala	
	30	35	40			
ttt gac aga	gaa aga atc	cct gaa agg	gtg gtg cat	gct aaa gga	agc	374
Phe Asp Arg	Glu Arg Ile	Pro Glu Arg	Val Val His	Ala Lys Gly	Ser	
	45	50	55		60	
gga gct tat	ggc act ttc	act gtg act	aaa gac atc	act aaa tac	act	422
Gly Ala Tyr	Gly Thr Phe	Thr Val Thr	Lys Asp Ile	Thr Lys Tyr	Thr	
	65	70		75		
aaa gcg aaa	att ttc tct	aaa gtg ggc	aaa aaa acc	gaa tgc ttc	ttc	470
Lys Ala Lys	Ile Phe Ser	Lys Val Gly	Lys Lys Thr	Glu Cys Phe	Phe	
	80	85		90		
aga ttt tct	act gtg gct	ggt gaa aga	ggc agt gcg	gat gcg gtg	aga	518
Arg Phe Ser	Thr Val Ala	Gly Glu Arg	Gly Ser Ala	Asp Ala Val	Arg	
	95	100		105		
gac cct aga	ggt ttt gcg	atg aag tat	tac act gaa	gaa ggt aac	tgg	566
Asp Pro Arg	Gly Phe Ala	Met Lys Tyr	Tyr Thr Glu	Glu Gly Asn	Trp	
	110	115		120		
gat tta gtg	ggg aac aac	acg cct gtt	ttc ttt atc	cgt gat gcg	atc	614
Asp Leu Val	Gly Asn Asn	Thr Pro Val	Phe Phe Ile	Arg Asp Ala	Ile	
	125	130		135	140	
aaa ttc cct	gat ttc atc	cac act caa	aaa cga gat	cct caa acc	aat	662
Lys Phe Pro	Asp Phe Ile	His Thr Gln	Lys Arg Asp	Pro Gln Thr	Asn	
	145	150		155		
ttg cct aac	cat gac atg	gta tgg gat	ttt tgg agt	aat gtt cct	gaa	710
Leu Pro Asn	His Asp Met	Val Trp Asp	Phe Trp Ser	Asn Val Pro	Glu	
	160	165		170		
agc tta tac	caa gta aca	tgg gtt atg	agc gat agg	ggt att cct	aaa	758
Ser Leu Tyr	Gln Val Thr	Trp Val Met	Ser Asp Arg	Gly Ile Pro	Lys	
	175	180		185		
tct ttc cgc	cac atg gat	ggt ttt ggc	agc cac act	ttc agt ctt	atc	806
Ser Phe Arg	His Met Asp	Gly Phe Gly	Ser His Thr	Phe Ser Leu	Ile	
	190	195		200		

09095913 060904

aac gcg aaa ggc gaa cgc ttt tgg gtg aaa ttc cac ttt cac acc atg	854
Asn Ala Lys Gly Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met	
205 210 215 220	
caa ggc gtt aag cat ttg act aac gaa gaa gcc gca gaa gtt agg aag	902
Gln Gly Val Lys His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys	
225 230 235	
tat gat ccg gat tcc aat caa agg gat tta ttc aat gcg atc gct aga	950
Tyr Asp Pro Asp Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg	
240 245 250	
ggg gat ttc cca aaa tgg aaa tta agc att caa gtg atg cca gaa gaa	998
Gly Asp Phe Pro Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu	
255 260 265	
gat gct aag aag tat cga ttc cat ccg ttt gat gta act aaa att tgg	1046
Asp Ala Lys Lys Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp	
270 275 280	
tat ctc caa gat tat cca ttg atg gaa gtg ggc att gtg gag ttg aat	1094
Tyr Leu Gln Asp Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn	
285 290 295 300	
aaa aat cct gaa aac tat ttc gca gaa gtg gaa caa gcg gca ttc agt	1142
Lys Asn Pro Glu Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser	
305 310 315	
ccg gct aat gtc gtt cct gga att ggc tat agc cct gat agg atg tta	1190
Pro Ala Asn Val Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu	
320 325 330	
caa ggg cgc ttg ttc tct tat gga gac aca cac cgc tac cgc tta ggc	1238
Gln Gly Arg Leu Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly	
335 340 345	
gtt aat tat cct caa ata ccg gtt aat aaa cca aga tgc cca ttc cac	1286
Val Asn Tyr Pro Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His	
350 355 360	
tct tct agc aga gat ggt tac atg caa aac gga tac tac ggc tct tta	1334
Ser Ser Ser Arg Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu	
365 370 375 380	
caa aac tat acg cct agc tca ttg cct ggc tat aaa gaa gat aag agc	1382
Gln Asn Tyr Thr Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser	
385 390 395	
gcg aga gat cct aag ttc aac tta gct cat att gag aaa gag ttt gaa	1430
Ala Arg Asp Pro Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu	
400 405 410	
gtg tgg aat tgg gat tac aga gct gat gat agc gat tac tac acc caa	1478
Val Trp Asn Trp Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln	
415 420 425	
cca ggt gat tac tac cgc tca ttg cca gct gat gaa aaa gaa agg ttg	1526
Pro Gly Asp Tyr Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu	

Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu Asp Ala Lys Lys
 260 265 270
 Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp Tyr Leu Gln Asp
 275 280 285
 Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn Lys Asn Pro Glu
 290 295 300
 Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser Pro Ala Asn Val
 305 310 315 320
 Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu Gln Gly Arg Leu
 325 330 335
 Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly Val Asn Tyr Pro
 340 345 350
 Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His Ser Ser Ser Arg
 355 360 365
 Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu Gln Asn Tyr Thr
 370 375 380
 Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser Ala Arg Asp Pro
 385 390 395 400
 Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu Val Trp Asn Trp
 405 410 415
 Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln Pro Gly Asp Tyr
 420 425 430
 Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu His Asp Thr Ile
 435 440 445
 Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile Val Asp Lys Gln
 450 455 460
 Leu Glu His Phe Lys Lys Ala Asp Pro Lys Tyr Ala Glu Gly Val Lys
 465 470 475 480
 Lys Ala Leu Glu Lys His Gln Lys Met Met Lys Asp Met His Gly Lys
 485 490 495
 Asp Met His His Thr Lys Lys Lys Lys
 500 505

<210> 77
 <211> 727
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (51)...(674)

<400> 77
 gaagcgtgcc aaacccgttg ccctttggcg tggagcttgc caaatattgg atg cat 56
 Met His
 1
 aac ggc ttt gtg aat atc aat aac gaa aaa atg tct aaa agt ttg ggg 104
 Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser Leu Gly
 5 10 15
 aat agc ttt ttt gtt aaa gac gct ctc aaa aac tat gat ggc gaa att 152
 Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly Glu Ile
 20 25 30
 ttg cgc aat tac tta cta ggg gtg cat tat cgc tct gtt ttg aat ttc 200
 Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu Asn Phe
 35 40 45 50

aat gaa gaa gac ttg tta gtg agt aaa aaa cgc ttg gat aaa atc tat	248
Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys Ile Tyr	
55 60 65	
cgt tta aaa cag cgc gtt tta ggg act ctt gga gga ata aat cca aac	296
Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn Pro Asn	
70 75 80	
ttt aaa aaa gaa att tta gag tgc atg caa gat gat tta aac gtt tct	344
Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn Val Ser	
85 90 95	
aaa gcg ttg agc gtt tta gaa agc atg ctt tct tcc act aat gaa aaa	392
Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn Glu Lys	
100 105 110	
ttg gat caa aac cct aaa aac aag gct tta aag ggc gaa att tta gcg	440
Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile Leu Ala	
115 120 125 130	
aat ttg aaa ttc ata gaa gaa ctg ctt ggc atc ggg ttt aaa gac cct	488
Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys Asp Pro	
135 140 145	
agc gcc tat ttc caa tta ggc gtg agt gaa agc gaa aaa caa gaa att	536
Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln Glu Ile	
150 155 160	
gaa aac aag ata gaa gaa aga aaa cgc gcc aaa gag cga aaa gat ttt	584
Glu Asn Lys Ile Glu Glu Arg Lys Arg Ala Lys Glu Arg Lys Asp Phe	
165 170 175	
tta aaa gcc gat agc atc aga gaa gag ctt ttg aaa caa aaa atc gct	632
Leu Lys Ala Asp Ser Ile Arg Glu Glu Leu Leu Lys Gln Lys Ile Ala	
180 185 190	
ttg atg gac acc cca caa ggc acg atc tgg gag aag ttt ttt	674
Leu Met Asp Thr Pro Gln Gly Thr Ile Trp Glu Lys Phe Phe	
195 200 205	
taaacacctc caattttacc tttttacaca ttctagcaac aacttttcagc att	727

<210> 78

<211> 208

<212> PRT

<213> Helicobacter pylori

<400> 78

Met His Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser	
1 5 10 15	
Leu Gly Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly	
20 25 30	
Glu Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu	
35 40 45	
Asn Phe Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys	
50 55 60	
Ile Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn	
65 70 75 80	
Pro Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn	

<400> 80
 Met Leu Thr Ile Glu Thr Ser Lys Lys Phe Asp Lys Asp Leu Lys Ile
 1 5 10 15
 Leu Val Lys Asn Gly Phe Asp Leu Lys Leu Leu Tyr Lys Val Val Gly
 20 25 30
 Asn Leu Ala Thr Glu Gln Pro Leu Ala Pro Lys Tyr Lys Asp His Pro
 35 40 45
 Leu Lys Gly Gly Leu Lys Asp Phe Arg Glu Cys His Leu Lys Pro Asp
 50 55 60
 Leu Leu Leu Val Tyr Gln Ile Lys Lys Gln Glu Asn Thr Leu Phe Leu
 65 70 75 80
 Val Arg Leu Gly Ser His Ser Glu Leu Phe
 85 90

<210> 81
 <211> 425
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (78)...(341)

<400> 81
 agatgtaggt aacaaagaga cagatttgat tgttgaggat ttttctagtt acagcaatga 60
 aagaaaaagg gcttttag gtg ttg aag ctc aat ctt aaa aaa tct ttt caa 110
 Val Leu Lys Leu Asn Leu Lys Lys Ser Phe Gln
 1 5 10
 aaa gat ttt gat aaa ttg ctt ttg aat ggg ttt gat gat agc gtt ttg 158
 Lys Asp Phe Asp Lys Leu Leu Leu Asn Gly Phe Asp Asp Ser Val Leu
 15 20 25
 aat gaa gtc att cta acc tta aga aaa aaa gaa ccg cta gat cca caa 206
 Asn Glu Val Ile Leu Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln
 30 35 40
 ttt caa gat cat gcc tta aag gga aag tgg aaa cct ttt agg gaa tgc 254
 Phe Gln Asp His Ala Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys
 45 50 55
 cac att aag cct gat gtt ttg ctt gtg tat tta gtg aaa gat gat gaa 302
 His Ile Lys Pro Asp Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu
 60 65 70 75
 ctg att ttg tta agg tta ggc agt cat agc gag ctg ttt taatccaccc 351
 Leu Ile Leu Leu Arg Leu Gly Ser His Ser Glu Leu Phe
 80 85
 acacccctta taacgcttaa accaaatcgc ttgcgctata atgaactgat attatatattt 411
 aaaaggaata aaca 425

<210> 82
 <211> 88
 <212> PRT
 <213> Helicobacter pylori

<400> 82
 Val Leu Lys Leu Asn Leu Lys Lys Ser Phe Gln Lys Asp Phe Asp Lys

1	5	10	15
Leu Leu Leu Asn Gly Phe Asp Asp Ser Val Leu Asn Glu Val Ile Leu			
20	25	30	
Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln Phe Gln Asp His Ala			
35	40	45	
Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys His Ile Lys Pro Asp			
50	55	60	
Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu Leu Ile Leu Leu Arg			
65	70	75	80
Leu Gly Ser His Ser Glu Leu Phe			
85			

<210> 83
 <211> 844
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (111)...(779)

<400> 83	
gtcgttatttc gcgcttaatg agaacagagg tttttaaaac tatgggtttcg ttttaggttta	60
attaaatttc gctacaatta aataaaaacg ataatttttag agagattggc atg caa	116
	Met Gln
	1
ggt tta tgg att tat cca gag gat aca gaa gtt tta ggg gtt gct tgt	164
Gly Leu Trp Ile Tyr Pro Glu Asp Thr Glu Val Leu Gly Val Ala Cys	
5 10 15	
aag agc ctt tta aaa gca cta acg cca cgc tat caa aaa gtc gcc ttg	212
Lys Ser Leu Leu Lys Ala Leu Thr Pro Arg Tyr Gln Lys Val Ala Leu	
20 25 30	
ttt tcg ccc att agt gga ggg tgt gag agc ttg gag gag tgc gag agc	260
Phe Ser Pro Ile Ser Gly Gly Cys Glu Ser Leu Glu Glu Cys Glu Ser	
35 40 45 50	
ttg aac cct tta gaa ttt cat agt gcg ata agc aaa caa aag gct tta	308
Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys Ala Leu	
55 60 65	
gag ctt gcg agc acc gct caa gaa gag tta cta ttt gaa acg att ctc	356
Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr Ile Leu	
70 75 80	
aaa cgc tat gat gaa tta caa tcc acg cat gat ttt gtc att aat ttg	404
Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile Asn Leu	
85 90 95	
ggg tgt gcg ccg aag ttt ttc tta aac gct cct tta gat tta aac acc	452
Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu Asn Thr	
100 105 110	
att tta gcc aag cat tta aac gct tct gtt gtg gct gtc gcg caa acg	500
Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala Gln Thr	
115 120 125 130	

210

215

220

<210> 85

<211> 821

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (79)...(753)

<400> 85

tatgcctgga	ggtttggtgt	ggatgcgtca	agataatttg	cgntacaac	cgcaatttaa	60
agccagaaat	tgggcaaa	atg tgg aat ttt aac acc gaa tac agc agt cag	111			
	Met Trp Asn Phe Asn Thr Glu Tyr Ser Ser Gln					
	1	5		10		
tat ttt gat ttt aga gcc gcc ggt ttt gtc caa ttg att tct aat tac	159					
Tyr Phe Asp Phe Arg Ala Ala Gly Phe Val Gln Leu Ile Ser Asn Tyr						
	15	20		25		
atc aat caa ttt tct tca acg ctt ttt gta acc aac ttg ccc gca caa	207					
Ile Asn Gln Phe Ser Ser Thr Leu Phe Val Thr Asn Leu Pro Ala Gln						
	30	35		40		
gat att att tat gtg cct ggt tat gaa gtt tca ggg acg gct aaa tac	255					
Asp Ile Ile Tyr Val Pro Gly Tyr Glu Val Ser Gly Thr Ala Lys Tyr						
	45	50		55		
aag ggc ttt tct tta ggc ttg agc gtg gcg cga tca tgg cct tct tta	303					
Lys Gly Phe Ser Leu Gly Leu Ser Val Ala Arg Ser Trp Pro Ser Leu						
	60	65		70		75
aag ggg cgt ttg atc gct gat gtg tat gaa ttg gcg gcc acg aca ggc	351					
Lys Gly Arg Leu Ile Ala Asp Val Tyr Glu Leu Ala Ala Thr Thr Gly						
	80	85		90		
aat gtg ttt att ttg acg gca agt tat aaa atc cca cgc act ggt ctt	399					
Asn Val Phe Ile Leu Thr Ala Ser Tyr Lys Ile Pro Arg Thr Gly Leu						
	95	100		105		
agc atc act tgg ctt tca cgc ttc gtt acg gat ttg agt tat tgc tct	447					
Ser Ile Thr Trp Leu Ser Arg Phe Val Thr Asp Leu Ser Tyr Cys Ser						
	110	115		120		
tat agc cct tat cgt aac ggc cct acg gat att gac aga cgg cct agt	495					
Tyr Ser Pro Tyr Arg Asn Gly Pro Thr Asp Ile Asp Arg Arg Pro Ser						
	125	130		135		
aat tgc cct aaa acg ccc ggg att ttt cat gtt cat aaa ccc ggt tat	543					
Asn Cys Pro Lys Thr Pro Gly Ile Phe His Val His Lys Pro Gly Tyr						
	140	145		150		155
ggg gtg agc agt ttt ttt gta acc tac aaa ccc acc tat aag aag ctt	591					
Gly Val Ser Ser Phe Phe Val Thr Tyr Lys Pro Thr Tyr Lys Lys Leu						
	160	165		170		
aaa ggg ttg agc ttg aat gcg gtg ttt aac aat gtt ttt aac caa caa	639					
Lys Gly Leu Ser Leu Asn Ala Val Phe Asn Asn Val Phe Asn Gln Gln						

175	180	185	
tat att gat caa gca agc ccg gtg atg agc cct gat gaa ccc aat caa			687
Tyr Ile Asp Gln Ala Ser Pro Val Met Ser Pro Asp Glu Pro Asn Gln			
190	195	200	
gac aaa tac gca aga ggc atg gca gag cct ggc ttt aac gct aga ttt			735
Asp Lys Tyr Ala Arg Gly Met Ala Glu Pro Gly Phe Asn Ala Arg Phe			
205	210	215	
gaa att tcc tat aag ttt taataatgga tctaaaaata aggatttcat			783
Glu Ile Ser Tyr Lys Phe			
220	225		
gggtagcgga tctaatacaaa aataaaacat tcttttaga			821

<210> 86
 <211> 225
 <212> PRT
 <213> Helicobacter pylori

<400> 86

Met Trp Asn Phe Asn Thr Glu Tyr Ser Ser Gln Tyr Phe Asp Phe Arg	
1 5 10 15	
Ala Ala Gly Phe Val Gln Leu Ile Ser Asn Tyr Ile Asn Gln Phe Ser	
20 25 30	
Ser Thr Leu Phe Val Thr Asn Leu Pro Ala Gln Asp Ile Ile Tyr Val	
35 40 45	
Pro Gly Tyr Glu Val Ser Gly Thr Ala Lys Tyr Lys Gly Phe Ser Leu	
50 55 60	
Gly Leu Ser Val Ala Arg Ser Trp Pro Ser Leu Lys Gly Arg Leu Ile	
65 70 75 80	
Ala Asp Val Tyr Glu Leu Ala Ala Thr Thr Gly Asn Val Phe Ile Leu	
85 90 95	
Thr Ala Ser Tyr Lys Ile Pro Arg Thr Gly Leu Ser Ile Thr Trp Leu	
100 105 110	
Ser Arg Phe Val Thr Asp Leu Ser Tyr Cys Ser Tyr Ser Pro Tyr Arg	
115 120 125	
Asn Gly Pro Thr Asp Ile Asp Arg Arg Pro Ser Asn Cys Pro Lys Thr	
130 135 140	
Pro Gly Ile Phe His Val His Lys Pro Gly Tyr Gly Val Ser Ser Phe	
145 150 155 160	
Phe Val Thr Tyr Lys Pro Thr Tyr Lys Lys Leu Lys Gly Leu Ser Leu	
165 170 175	
Asn Ala Val Phe Asn Asn Val Phe Asn Gln Gln Tyr Ile Asp Gln Ala	
180 185 190	
Ser Pro Val Met Ser Pro Asp Glu Pro Asn Gln Asp Lys Tyr Ala Arg	
195 200 205	
Gly Met Ala Glu Pro Gly Phe Asn Ala Arg Phe Glu Ile Ser Tyr Lys	
210 215 220	
Phe	
225	

<210> 87
 <211> 1350
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS
 <222> (60)...(1202)

<400> 87

aaattttgaaa acattgactc agttttcgctc tcaagggcgt ttaattcaag gatcaaagc	59
atg aat tta aat ttt atg ccc cta ttg cat gct tat aac cat gcg agc	107
Met Asn Leu Asn Phe Met Pro Leu Leu His Ala Tyr Asn His Ala Ser	
1 5 10 15	
att gat ttt cat ttc aat tct agt gct agg gat ttt tgc gtg cat gaa	155
Ile Asp Phe His Phe Asn Ser Ser Ala Arg Asp Phe Cys Val His Glu	
20 25 30	
gtg cct ttg tat gaa ttt agt aac acg ggc gaa cat gcc gtt att caa	203
Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln	
35 40 45	
gtg agg aaa agc ggt tta agc act tta gaa atg ctt cag att ttt tct	251
Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser	
50 55 60	
caa att tta ggg gta aga atc gct gaa ttg ggt tat gcg ggc ttg aaa	299
Gln Ile Leu Gly Val Arg Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys	
65 70 75 80	
gat aaa aac gcg ctg acg act caa ttc atc tca ctc cct aaa aaa tac	347
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr	
85 90 95	
gcc cct tta tta gaa aaa aat acg agc aac ttt caa gaa aaa aac ctt	395
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Lys Asn Leu	
100 105 110	
aaa atc ctg tct ttg aat tac cac cac aat aaa atc aaa ttg ggg cat	443
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His	
115 120 125	
ttg aaa ggg aat cgc ttt ttt atg cgt ttt aaa aaa atg acc cct cta	491
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu	
130 135 140	
aac gct caa aaa aca aag cag gtt tta gaa caa atc gcg cag ttt gga	539
Asn Ala Gln Lys Thr Lys Gln Val Leu Glu Gln Ile Ala Gln Phe Gly	
145 150 155 160	
atg cct aat tat ttt ggc tcg caa cgc ttt ggg aag ttc aat gac aac	587
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn	
165 170 175	
cac caa gag ggt tta aaa atc tta caa aat caa acg aaa ttc gcc cat	635
His Gln Glu Gly Leu Lys Ile Leu Gln Asn Gln Thr Lys Phe Ala His	
180 185 190	
caa aaa tta aac gct ttt tta att tca agc tat caa agt tat ttg ttt	683
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe	
195 200 205	
aac gcg ctt tta agc aaa cga tta gaa atc agt aaa atc att agc gct	731
Asn Ala Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala	

210	215	220	
ttt agt gtc aaa gaa aat tta gaa ttt ttt aaa caa aaa aat tta agc			779
Phe Ser Val Lys Glu Asn Leu Glu Phe Phe Lys Gln Lys Asn Leu Ser			
225	230	235	240
ggt gat tca gac act cta aaa acc ctt aaa aac caa gcc cac ccc ttt			827
Val Asp Ser Asp Thr Leu Lys Thr Leu Lys Asn Gln Ala His Pro Phe			
	245	250	255
aaa atc tta gaa ggc gat gtg atg tgc cat tac cct tat ggg aag ttt			875
Lys Ile Leu Glu Gly Asp Val Met Cys His Tyr Pro Tyr Gly Lys Phe			
	260	265	270
ttt gac gct tta gaa tta gaa aaa gag ggc gaa agg ttt ttg aaa aaa			923
Phe Asp Ala Leu Glu Leu Glu Lys Glu Gly Glu Arg Phe Leu Lys Lys			
	275	280	285
gaa gtt gcg cct acg ggg tta cta gac ggc aaa aaa gct ctt tat gca			971
Glu Val Ala Pro Thr Gly Leu Leu Asp Gly Lys Lys Ala Leu Tyr Ala			
	290	295	300
aaa aat ttg agt tta gaa att gaa aaa gaa ttc cag cat aac ctt tta			1019
Lys Asn Leu Ser Leu Glu Ile Glu Lys Glu Phe Gln His Asn Leu Leu			
	305	310	315
agt agc cat gct aaa acg cta ggc tct agg cgg ttt ttt tgg gtg ttt			1067
Ser Ser His Ala Lys Thr Leu Gly Ser Arg Arg Phe Phe Trp Val Phe			
	325	330	335
gta gaa aat gta act tct caa tac gtg aaa gaa aaa gcg caa ttt gaa			1115
Val Glu Asn Val Thr Ser Gln Tyr Val Lys Glu Lys Ala Gln Phe Glu			
	340	345	350
ttg gga ttt tac ttg cct aaa ggg agt tat gcg agc gcg ttg ctc aaa			1163
Leu Gly Phe Tyr Leu Pro Lys Gly Ser Tyr Ala Ser Ala Leu Leu Lys			
	355	360	365
gaa atc aag cat gag aaa gga gaa aat aat gac gaa ttt tgaaaagatt			1212
Glu Ile Lys His Glu Lys Gly Glu Asn Asn Asp Glu Phe			
	370	375	380
atcgcgcaaa acaggatcaa aacgaacgcg gtttttagcga cttattgcgt gatttttgct			1272
tttatcgggg tggttggtgga tgtcattaga attaattgcta atgatttagg aatagctctt			1332
tttaaaactca tgactttt			1350

<210> 88
 <211> 381
 <212> PRT
 <213> Helicobacter pylori

<400> 88
 Met Asn Leu Asn Phe Met Pro Leu Leu His Ala Tyr Asn His Ala Ser
 1 5 10 15
 Ile Asp Phe His Phe Asn Ser Ser Ala Arg Asp Phe Cys Val His Glu
 20 25 30
 Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln
 35 40 45
 Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser

	50					55					60					
Gln 65	Ile	Leu	Gly	Val	Arg 70	Ile	Ala	Glu	Leu	Gly 75	Tyr	Ala	Gly	Leu	Lys 80	
Asp	Lys	Asn	Ala	Leu 85	Thr	Thr	Gln	Phe	Ile 90	Ser	Leu	Pro	Lys	Lys 95	Tyr	
Ala	Pro	Leu	Leu 100	Glu	Lys	Asn	Thr	Ser 105	Asn	Phe	Gln	Glu	Lys 110	Asn	Leu	
Lys	Ile	Leu 115	Ser	Leu	Asn	Tyr	His 120	His	Asn	Lys	Ile	Lys 125	Leu	Gly	His	
Leu	Lys 130	Gly	Asn	Arg	Phe	Phe 135	Met	Arg	Phe	Lys	Lys 140	Met	Thr	Pro	Leu	
Asn 145	Ala	Gln	Lys	Thr	Lys 150	Gln	Val	Leu	Glu	Gln 155	Ile	Ala	Gln	Phe	Gly 160	
Met	Pro	Asn	Tyr	Phe 165	Gly	Ser	Gln	Arg	Phe 170	Gly	Lys	Phe	Asn	Asp 175	Asn	
His	Gln	Glu	Gly 180	Leu	Lys	Ile	Leu	Gln 185	Asn	Gln	Thr	Lys	Phe 190	Ala	His	
Gln	Lys	Leu 195	Asn	Ala	Phe	Leu	Ile 200	Ser	Ser	Tyr	Gln	Ser 205	Tyr	Leu	Phe	
Asn	Ala 210	Leu	Leu	Ser	Lys 215	Arg	Leu	Glu	Ile	Ser	Lys 220	Ile	Ile	Ser	Ala	
Phe 225	Ser	Val	Lys	Glu	Asn 230	Leu	Glu	Phe	Phe	Lys 235	Gln	Lys	Asn	Leu	Ser 240	
Val	Asp	Ser	Asp	Thr 245	Leu	Lys	Thr	Leu	Lys 250	Asn	Gln	Ala	His	Pro 255	Phe	
Lys	Ile	Leu	Glu 260	Gly	Asp	Val	Met	Cys 265	His	Tyr	Pro	Tyr	Gly 270	Lys	Phe	
Phe	Asp	Ala 275	Leu	Glu	Leu	Glu	Lys 280	Glu	Gly	Glu	Arg	Phe 285	Leu	Lys	Lys	
Glu	Val 290	Ala	Pro	Thr	Gly	Leu 295	Leu	Asp	Gly	Lys	Lys 300	Ala	Leu	Tyr	Ala	
Lys 305	Asn	Leu	Ser	Leu	Glu 310	Ile	Glu	Lys	Glu	Phe 315	Gln	His	Asn	Leu	Leu 320	
Ser	Ser	His	Ala	Lys 325	Thr	Leu	Gly	Ser	Arg 330	Arg	Phe	Phe	Trp	Val 335	Phe	
Val	Glu	Asn	Val 340	Thr	Ser	Gln	Tyr	Val 345	Lys	Glu	Lys	Ala	Gln 350	Phe	Glu	
Leu	Gly	Phe 355	Tyr	Leu	Pro	Lys	Gly 360	Ser	Tyr	Ala	Ser	Ala 365	Leu	Leu	Lys	
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-97-

09695913-062901

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ctt aca ggc ggg gag cca agc ttg tat ttc aat aac cct att tta atc Leu Thr Gly Gly Glu Pro Ser Leu Tyr Phe Asn Asn Pro Ile Leu Ile 95 100 105			399
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g c c t a g t a t t a g c g g g t t c g t t c a a a a a t t g c g c g a g c a t g c g g g g a a t t t t t t g a a t 1008
g a g a g a g g g t a a c a a g c t c a t t g g g a t t t g t g g c t t a a t c c t a t c a a t c a a c a g a a g c 1068
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35 40 45
Leu Thr Gly Cys Asp Ser Leu Tyr Ala Val His Pro Lys Phe Lys Thr
50 55 60
Ser Trp Asp Tyr Tyr Asn Glu Pro Lys Pro Leu Ile Glu Arg Leu Glu
65 70 75 80
Asp Leu Ala Pro Asn Tyr Lys Asp Phe Asp Phe Ile Leu Thr Gly Gly
85 90 95
Glu Pro Ser Leu Tyr Phe Asn Asn Pro Ile Leu Ile Ser Val Leu Glu
100 105 110
His Phe Tyr Arg Gln Lys Ile Pro Leu Cys Val Glu Ser Asn Gly Ser
115 120 125
Ile Phe Phe Glu Phe Ser Pro Ile Leu Lys Glu Leu His Phe Thr Leu
130 135 140
Ser Val Lys Leu Ser Phe Ser Leu Glu Glu Glu Ser Lys Arg Ile His
145 150 155 160
Leu Lys Ala Leu Gln Asn Ile Leu Asn Asn Ala Lys Ser Ala His Phe
165 170 175
Lys Phe Val Leu Glu Ser Gln Asn Ala Ala Gln Ser Ile Ile Glu Ile
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Gln Ser Leu Leu Lys Gln Leu Ser Leu Lys Asn Asn Glu Ile Phe Leu
195 200 205
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g a t t t t a t t c g g t g g g a t t g t c a g c a t c a a g c c t c a t t g t t c c t a t t a g c g t t a t t t t a 119
a t g g t g g t t t t a c t a a a a g a g t c g c a c t c t c g t t a t t t g t g g g c a t t 167
Met Val Val Phe Thr Lys Arg Val Ala Leu Ser Leu Phe Val Gly Ile
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gaa	tat	att	tat	cat	aaa	atc	act	tcc	gtt	ttt	tac	act	tac	gag	cca	263
Glu	Tyr	Ile	Tyr	His	Lys	Ile	Thr	Ser	Val	Phe	Tyr	Thr	Tyr	Glu	Pro	
			35				40						45			
gaa	aag	ggg	ctt	aat	ttc	aat	ctt	tcc	aac	ctc	tat	gtt	ttt	ggg	ttt	311
Glu	Lys	Gly	Leu	Asn	Phe	Asn	Leu	Ser	Asn	Leu	Tyr	Val	Phe	Gly	Phe	
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Leu	Ile	Phe	Leu	Gly	Val	Leu	Ser	Gln	Val	Ile	Leu	Lys	Ser	Gly	Ser	
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gtg	caa	aac	ttt	gtc	aaa	aaa	gct	aaa	aaa	tac	tca	aaa	aac	gct	aaa	407
Val	Gln	Asn	Phe	Val	Lys	Lys	Ala	Lys	Lys	Tyr	Ser	Lys	Asn	Ala	Lys	
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act	ccc	gaa	ttt	atc	gcc	ttt	ttt	tca	ggg	atc	att	att	ttt	gta	gat	455
Thr	Pro	Glu	Phe	Ile	Ala	Phe	Phe	Ser	Gly	Ile	Ile	Ile	Phe	Val	Asp	
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Asp	Tyr	Phe	Asn	Ala	Leu	Thr	Val	Gly	Gln	Ile	Ser	Lys	Ser	Leu	Asn	
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Tyr	Ile	Met	Gly	Ile	Met	Asn	Asn	Asp	Ser	Ser	Pro	Leu	Leu	Lys	Asp	
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Ser	Phe	Ser	Val	Leu	Val	Gln	Ser	Leu	Ser	Ser	Asn	Tyr	Tyr	Ala	Ile	
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cct	agc	atg	aga	aag	tat	caa	aac	ata	ggc	gtg	aag	gat	ttt	tat	agc	791
Pro	Ser	Met	Arg	Lys	Tyr	Gln	Asn	Ile	Gly	Val	Lys	Asp	Phe	Tyr	Ser	
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Glu	Gln	Glu	Glu	Ser	Ser	Ser	Lys	Leu	Ala	Pro	Leu	Ser	Leu	Leu	Pro	
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Leu	Ser	Ile	Leu	Leu												

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Thr	Gly	Val	Ile	Leu	Lys	Asn	Thr	Asp	Ala	Ser	Phe	Ser	Leu	Phe	Tyr															
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			420					425					430																	
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Thr	Ile	Ala	Met	Leu	Cys	Ser	Ala	Val	Ser	Leu	Gly	Val	Ala	Ser	Phe															
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1679
 1710

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 Val Gln Asn Phe Val Lys Lys Ala Lys Lys Tyr Ser Lys Asn Ala Lys
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 Thr Pro Glu Phe Ile Ala Phe Phe Ser Gly Ile Ile Ile Phe Val Asp
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 Asp Tyr Phe Asn Ala Leu Thr Val Gly Gln Ile Ser Lys Ser Leu Asn
 115 120 125
 Asp Ala His Asn Ser Thr Arg Glu Arg Leu Ala Tyr Ile Ile Asp Ser
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 Tyr Ile Met Gly Ile Met Asn Asn Asp Ser Ser Pro Leu Leu Lys Asp
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 Ser Phe Ser Val Leu Val Gln Ser Leu Ser Ser Asn Tyr Tyr Ala Ile
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 Phe Ala Leu Ile Ala Val Phe Leu Thr Ile Leu Trp Gln Ile Asn Leu
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 Pro Ser Met Arg Lys Tyr Gln Asn Ile Gly Val Lys Asp Phe Tyr Ser
 210 215 220
 Glu Gln Glu Glu Ser Ser Ser Lys Leu Ala Pro Leu Ser Leu Leu Pro
 225 230 235 240
 Leu Ser Ile Leu Leu Ile Val Ser Ile Ser Ser Leu Leu Phe Tyr
 245 250 255
 Thr Gly Val Ile Leu Lys Asn Thr Asp Ala Ser Phe Ser Leu Phe Tyr
 260 265 270
 Gly Gly Leu Phe Ser Leu Ile Val Thr Tyr Leu Leu Ala Tyr Lys Phe
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 Leu Glu Lys Gly Ser Phe Phe Lys Leu Met Leu Asp Gly Phe Lys Ser
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 Val Gly Pro Ala Ile Leu Val Leu Thr Leu Ala Trp Ala Ile Gly Pro
 305 310 315 320
 Val Ile Arg Asp Asp Ala Gln Thr Gly Leu Tyr Leu Ala Asn Ile Ser
 325 330 335
 Lys Gly Phe Leu Asn Asn Gly Gly Gly Val Tyr Met Pro Leu Ile Phe
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 Phe Leu Ile Ser Gly Phe Ile Ala Phe Ser Thr Gly Thr Ser Trp Gly
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 Ala Phe Ala Ile Met Leu Pro Ile Gly Ala Gly Met Ala Ser Glu Ser
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 Asp Ile Ile Leu Ile Val Ser Ala Ile Leu Ser Gly Ala Val Tyr Gly
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090901 062901

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 Ile Ser Leu Ser Val Lys His Thr Asp Asn
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 Val Ile Ser Leu Arg Lys Glu Asn Gly Val Arg Thr Leu Ile Ser Leu
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 Gly Ile Leu Leu Ser Val Leu Ser Gly Asp Asp Leu Lys Leu Tyr Ser
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 75 80 85 90
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 ttc cat att aaa ttg cct gaa ggc gct cct agc aac ttc aaa tca ggt 495
 Phe His Ile Lys Leu Pro Glu Gly Ala Pro Ser Asn Phe Lys Ser Gly
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[illegible]

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atc gcc tta cac cct aaa gct caa agg ggc gat agc ttt gcg ttt agt 355
Ile Ala Leu His Pro Lys Ala Gln Arg Gly Asp Ser Phe Ala Phe Ser
75 80 85

aaa atg tta gaa aat cat ctt aat att aat ttt ttt atc gct gga gcg 403
Lys Met Leu Glu Asn His Leu Asn Ile Asn Phe Phe Ile Ala Gly Ala
90 95 100

tat ggg ttt gaa gaa aat ttt tta aag gat tgt caa gct tgg agt ttg 451
Tyr Gly Phe Glu Glu Asn Phe Leu Lys Asp Cys Gln Ala Trp Ser Leu
105 110 115

agc gag atg act ttt agc cat gaa gtg gct aaa att gtc tta tgc gag 499
Ser Glu Met Thr Phe Ser His Glu Val Ala Lys Ile Val Leu Cys Glu
120 125 130

caa atc tat agg gct tta agc att att ttt aag cat cca tac cat aaa 547
Gln Ile Tyr Arg Ala Leu Ser Ile Ile Phe Lys His Pro Tyr His Lys
135 140 145 150

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35 40 45
Lys Lys Leu Ala Gln Lys Ser Tyr Ser Leu Ala Phe Glu Pro Tyr Leu
50 55 60
Asn Pro Lys Ala Lys Asn Ile Ala Leu His Pro Lys Ala Gln Arg Gly
65 70 75 80
Asp Ser Phe Ala Phe Ser Lys Met Leu Glu Asn His Leu Asn Ile Asn
85 90 95
Phe Phe Ile Ala Gly Ala Tyr Gly Phe Glu Glu Asn Phe Leu Lys Asp
100 105 110
Cys Gln Ala Trp Ser Leu Ser Glu Met Thr Phe Ser His Glu Val Ala
115 120 125
Lys Ile Val Leu Cys Glu Gln Ile Tyr Arg Ala Leu Ser Ile Ile Phe
130 135 140
Lys His Pro Tyr His Lys
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<400> 97

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agcaaaactt ggatacaatc ctaacaaaac tgcaaaatta aggaaaaac atg gga ttt	118
Met Gly Phe	
1	
gca gat ttc ttt aaa aat ttt aag atc aat aaa ttg cgg aca gcg cca	166
Ala Asp Phe Phe Lys Asn Phe Lys Ile Asn Lys Leu Arg Thr Ala Pro	
5 10 15	
agt aag gaa gaa cag cca agc cat tgg gtg aaa tgc cct aaa tgt tat	214
Ser Lys Glu Glu Gln Pro Ser His Trp Val Lys Cys Pro Lys Cys Tyr	
20 25 30 35	
gcg tta atg tat cat aaa gaa gtg ttt agt aaa tac agc gtg tgt ttg	262
Ala Leu Met Tyr His Lys Glu Val Phe Ser Lys Tyr Ser Val Cys Leu	
40 45 50	
aaa tgc cat tac cat ttc cgc atg aaa gcg gct gaa agg att gaa ttt	310
Lys Cys His Tyr His Phe Arg Met Lys Ala Ala Glu Arg Ile Glu Phe	
55 60 65	
tta tgc gat gtg ggg agt ttt gaa gag ttt gac aag cat tta cgg cct	358
Leu Cys Asp Val Gly Ser Phe Glu Glu Phe Asp Lys His Leu Arg Pro	
70 75 80	
aat gat cct tta aat ttc gtg gat aaa gag agc tat aaa caa cgc att	406
Asn Asp Pro Leu Asn Phe Val Asp Lys Glu Ser Tyr Lys Gln Arg Ile	
85 90 95	
aaa aaa tac gaa aaa agg act aac cgc cca agc tca gtg atc agc ggt	454
Lys Lys Tyr Glu Lys Arg Thr Asn Arg Pro Ser Ser Val Ile Ser Gly	
100 105 110 115	
gag gct aaa atc aac cgc atg cct ttg cag atc gtg gtg ttt gat ttt	502
Glu Ala Lys Ile Asn Arg Met Pro Leu Gln Ile Val Val Phe Asp Phe	
120 125 130	
agc ttt atg ggg ggg agt tta ggc tct gtg gag ggc gaa aag atc gta	550
Ser Phe Met Gly Gly Ser Leu Gly Ser Val Glu Gly Glu Lys Ile Val	
135 140 145	
aga gca atc aat cgc gcg gtc gct aaa aga gaa gcg tta ttg att gtt	598
Arg Ala Ile Asn Arg Ala Val Ala Lys Arg Glu Ala Leu Leu Ile Val	
150 155 160	
tca gcg agt ggg ggg gct agg atg caa gaa tcc act tat tcg ctc atg	646
Ser Ala Ser Gly Gly Ala Arg Met Gln Glu Ser Thr Tyr Ser Leu Met	
165 170 175	
caa atg gct aaa acg agc gcg gct ttg aac cga ttg agt gag gcc aaa	694
Gln Met Ala Lys Thr Ser Ala Ala Leu Asn Arg Leu Ser Glu Ala Lys	
180 185 190 195	
ctc cct ttc att tcg ctc tta agc gat ccc act tat ggg ggc gtt agc	742

210	215	220
Pro Gly Ala Met Ile Gly	Phe Ala Gly Pro Arg	Val Ile Lys Gln Thr
225	230	235
Ile Gly Ala Asp Leu Pro	Glu Gly Phe Gln Thr	Ala Glu Phe Leu Leu
245	250	255
Glu His Gly Leu Ile Asp	Met Ile Val His Arg	Lys Asp Leu Lys Lys
260	265	270
Thr Leu Ser Asp Leu Ile	Ala Met Met Thr His	Lys Thr Ser Lys Ile
275	280	285
Phe		

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 <213> Helicobacter pylori

<220>
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gcttataata aacaaaatta gcttaagagt agtg atg caa ggg ttt ctt tta caa	115
Met Gln Gly Phe Leu Leu Gln	
1 5	
aca caa agc ata aga gat gaa gat ttg atc gtg cgc gtt tta acc aaa	163
Thr Gln Ser Ile Arg Asp Glu Asp Leu Ile Val Arg Val Leu Thr Lys	
10 15 20	
aac cag ctc aaa acc ctc tat cgt ttc tat ggc aaa cgc cat agc gtg	211
Asn Gln Leu Lys Thr Leu Tyr Arg Phe Tyr Gly Lys Arg His Ser Val	
25 30 35	
ctg aat gtg ggg cgt aaa att gat ttt gaa gaa gaa aac gat gat aag	259
Leu Asn Val Gly Arg Lys Ile Asp Phe Glu Glu Glu Asn Asp Asp Lys	
40 45 50 55	
ttt tta ccc aag tta agg aat att ttg cat tta ggc tat att tgg gaa	307
Phe Leu Pro Lys Leu Arg Asn Ile Leu His Leu Gly Tyr Ile Trp Glu	
60 65 70	
aga gaa atg gag cgc ttg ttt ttt tgg caa cgc ttt tgc gct ctc ttg	355
Arg Glu Met Glu Arg Leu Phe Phe Trp Gln Arg Phe Cys Ala Leu Leu	
75 80 85	
ttt agg cat tta gaa ggc gtg cat tct tta gat agc gtc tat ttt gac	403
Phe Arg His Leu Glu Gly Val His Ser Leu Asp Ser Val Tyr Phe Asp	
90 95 100	
act tta gat gat ggg gct aac aaa ctc gcc aaa cag cac ccc tta aga	451
Thr Leu Asp Asp Gly Ala Asn Lys Leu Ala Lys Gln His Pro Leu Arg	
105 110 115	
gtg att tta gaa atg tat gca acg ctt ttg aat ttt gaa ggg cgc ttg	499
Val Ile Leu Glu Met Tyr Ala Thr Leu Leu Asn Phe Glu Gly Arg Leu	
120 125 130 135	

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caa agt tac aat tct tgt ttt tta tgc gat gca aaa tta gag cgt tct	547
Gln Ser Tyr Asn Ser Cys Phe Leu Cys Asp Ala Lys Leu Glu Arg Ser	
140 145 150	
gtc gct tta gcg caa ggg ttt att cta gcg cac ccc tct tgt ttg aaa	595
Val Ala Leu Ala Gln Gly Phe Ile Leu Ala His Pro Ser Cys Leu Lys	
155 160 165	
gct aaa agc cta aat tta gaa aaa atc caa gct ttt ttt cgc act caa	643
Ala Lys Ser Leu Asn Leu Glu Lys Ile Gln Ala Phe Phe Arg Thr Gln	
170 175 180	
agc acg att gat tta gaa aca gaa gaa gta gaa gaa tta tgg cgc acg	691
Ser Thr Ile Asp Leu Glu Thr Glu Glu Val Glu Glu Leu Trp Arg Thr	
185 190 195	
ctg aat tta ggg ttt tgaaaggta aaaatgaaat ttaaattttt gaatatggat	746
Leu Asn Leu Gly Phe	
200	
aatgaaagcg gttttatttt gattgaaaaa gaattgaaac gattaaacat tctcgctcaa	806
gtca	810

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 <213> Helicobacter pylori

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20 25 30	
Tyr Gly Lys Arg His Ser Val Leu Asn Val Gly Arg Lys Ile Asp Phe	
35 40 45	
Glu Glu Glu Asn Asp Asp Lys Phe Leu Pro Lys Leu Arg Asn Ile Leu	
50 55 60	
His Leu Gly Tyr Ile Trp Glu Arg Glu Met Glu Arg Leu Phe Phe Trp	
65 70 75 80	
Gln Arg Phe Cys Ala Leu Leu Phe Arg His Leu Glu Gly Val His Ser	
85 90 95	
Leu Asp Ser Val Tyr Phe Asp Thr Leu Asp Asp Gly Ala Asn Lys Leu	
100 105 110	
Ala Lys Gln His Pro Leu Arg Val Ile Leu Glu Met Tyr Ala Thr Leu	
115 120 125	
Leu Asn Phe Glu Gly Arg Leu Gln Ser Tyr Asn Ser Cys Phe Leu Cys	
130 135 140	
Asp Ala Lys Leu Glu Arg Ser Val Ala Leu Ala Gln Gly Phe Ile Leu	
145 150 155 160	
Ala His Pro Ser Cys Leu Lys Ala Lys Ser Leu Asn Leu Glu Lys Ile	
165 170 175	
Gln Ala Phe Phe Arg Thr Gln Ser Thr Ile Asp Leu Glu Thr Glu Glu	
180 185 190	
Val Glu Glu Leu Trp Arg Thr Leu Asn Leu Gly Phe	
195 200	

<210> 101
 <211> 999
 <212> DNA

[illegible]

<221> CDS

<222> (76) ... (927)

<400> 101

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 Leu Met Val Met Trp Ala Lys Lys His Thr Lys Thr His Gly Leu Leu
 205 210 215 220

att gtg gtt tat ggt ttg ggg tat tcc ttg atg cgc ttt att gcg gaa 783
 Ile Val Val Tyr Gly Leu Gly Tyr Ser Leu Met Arg Phe Ile Ala Glu
 225 230 235

ttt tac aga gag ccg gac agc caa atg ggg gtt tat ttt tta aat ttg 831
 Phe Tyr Arg Glu Pro Asp Ser Gln Met Gly Val Tyr Phe Leu Asn Leu
 240 245 250

agc atg ggg cag att tta agc tta ttt atg gta att gtt tcg tta ggg 879
 Ser Met Gly Gln Ile Leu Ser Leu Phe Met Val Ile Val Ser Leu Gly
 255 260 265

att tta ttg tat gct aca aaa aat tct aaa aaa ata aag gaa aat caa 927
 Ile Leu Leu Tyr Ala Thr Lys Asn Ser Lys Lys Ile Lys Glu Asn Gln
 270 275 280

tgaatttttt ggatcaagaa aaaagaagac aattattataa cgagcgccat tcttgcaaga 987
 tgtttgatag cc 999

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 <212> PRT
 <213> Helicobacter pylori

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 Ala Ile Val Thr Ala Phe Tyr Met Ala Leu Arg Met Ile Gln Lys Asp
 35 40 45
 Pro Lys Arg Phe Pro Ile Glu Arg Lys Glu Phe Glu Ser Tyr Phe Leu
 50 55 60
 Trp Ala Glu Leu Gly Ile Val Leu Gly Ala Arg Ile Gly Tyr Ile Leu
 65 70 75 80
 Ile Tyr Glu Pro Asn Ser Gly Tyr Tyr Leu Thr His Phe Trp Gln Ile
 85 90 95
 Phe Asn Pro Phe Asp Ser His Gly Asn Phe Val Gly Ile Arg Gly Met
 100 105 110
 Ser Tyr His Gly Gly Leu Val Gly Phe Leu Ile Ala Ser Tyr Leu Tyr
 115 120 125
 Ser Arg Lys Asp Leu Lys Lys Leu Leu Ile Tyr Leu Asp Leu Ile Ala
 130 135 140
 Ile Ser Leu Pro Leu Gly Tyr Val Phe Gly Arg Ile Gly Asn Phe Leu
 145 150 155 160
 Asn Gln Glu Leu Val Gly Arg Ile Val Pro Lys Asp Ser His Leu Gly
 165 170 175
 Gln Ile Ile Gly Ile Met Val Asp Asn Glu Leu Arg Tyr Pro Ser Gln
 180 185 190
 Leu Ile Glu Ala Phe Leu Glu Gly Val Ile Val Phe Leu Met Val Met
 195 200 205
 Trp Ala Lys Lys His Thr Lys Thr His Gly Leu Leu Ile Val Val Tyr
 210 215 220
 Gly Leu Gly Tyr Ser Leu Met Arg Phe Ile Ala Glu Phe Tyr Arg Glu

att cct gta gag atc act tac ggc tta gaa aga tta gcg atg tat gtg 592
 Ile Pro Val Glu Ile Thr Tyr Gly Leu Glu Arg Leu Ala Met Tyr Val
 155 160 165

caa aaa gtg gaa aat atc cta gag att gaa tgg gct aaa aaa aat cat 640
 Gln Lys Val Glu Asn Ile Leu Glu Ile Glu Trp Ala Lys Lys Asn His
 170 175 180 185

gac agc gtg aat tac gca caa gtg cat ttg gaa agc gaa tac gaa ttc 688
 Asp Ser Val Asn Tyr Ala Gln Val His Leu Glu Ser Glu Tyr Glu Phe
 190 195 200

agc aag tat cat ttt gaa aca gcg agc gtg aaa cgg cta tta gaa atg 736
 Ser Lys Tyr His Phe Glu Thr Ala Ser Val Lys Arg Leu Leu Glu Met
 205 210 215

ttt aaa aac gct caa gcc gaa gcc ttg cat tgc ttg gaa aac aag ctc 784
 Phe Lys Asn Ala Gln Ala Glu Ala Leu His Cys Leu Glu Asn Lys Leu
 220 225 230

ccc ttg ccg gct tat gat ttt gtg atg tta tgc tcg cat ttt ttc aat 832
 Pro Leu Pro Ala Tyr Asp Phe Val Met Leu Cys Ser His Phe Phe Asn
 235 240 245

att tta gac gcc aga aaa gcg att tcg gtg gct gaa agg caa aat tat 880
 Ile Leu Asp Ala Arg Lys Ala Ile Ser Val Ala Glu Arg Gln Asn Tyr
 250 255 260 265

att tta caa atc agg gat tta gcc aaa ggg tgt gcg ctt ctt tat aaa 928
 Ile Leu Gln Ile Arg Asp Leu Ala Lys Gly Cys Ala Leu Leu Tyr Lys
 270 275 280

gaa caa gaa gaa gag agg gaa gag cgt tta aaa aac gct tta aca aag 976
 Glu Gln Glu Glu Glu Arg Glu Glu Arg Leu Lys Asn Ala Leu Thr Lys
 285 290 295

gct gaa aat ggc gtt agt taaggaagtg ttggtagttt tgaatcgcct 1024
 Ala Glu Asn Gly Val Ser
 300

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 tagtgaattt agcgagattg 1104

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 <211> 303
 <212> PRT
 <213> Helicobacter pylori

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 20 25 30
 Gly Thr Phe His Pro Ala Thr Leu Leu Arg Ser Leu Asp Lys Lys Pro
 35 40 45
 Trp Asn Val Ala Tyr Val Ala Pro Ser Arg Arg Pro Thr Asp Gly Arg
 50 55 60
 Tyr Gly Glu Asn Pro Asn Arg Leu Gly Ser Tyr Tyr Gln Phe Gln Val
 65 70 75 80

Val Ile Lys Pro Ser Pro Ser Asn Ile Gln Glu Leu Tyr Leu Lys Ser
85 90 95
Leu Glu Val Leu Gly Ile Asn Leu Asn Glu His Asp Ile Arg Phe Val
100 105 110
Glu Asp Asn Trp Glu Ser Pro Thr Leu Gly Ala Trp Gly Leu Gly Trp
115 120 125
Glu Val Trp Leu Asp Gly Met Glu Val Thr Gln Phe Thr Tyr Phe Gln
130 135 140
Gln Val Gly Gly Ile Ala Cys Ser Pro Ile Pro Val Glu Ile Thr Tyr
145 150 155 160
Gly Leu Glu Arg Leu Ala Met Tyr Val Gln Lys Val Glu Asn Ile Leu
165 170 175
Glu Ile Glu Trp Ala Lys Lys Asn His Asp Ser Val Asn Tyr Ala Gln
180 185 190
Val His Leu Glu Ser Glu Tyr Glu Phe Ser Lys Tyr His Phe Glu Thr
195 200 205
Ala Ser Val Lys Arg Leu Leu Glu Met Phe Lys Asn Ala Gln Ala Glu
210 215 220
Ala Leu His Cys Leu Glu Asn Lys Leu Pro Leu Pro Ala Tyr Asp Phe
225 230 235 240
Val Met Leu Cys Ser His Phe Phe Asn Ile Leu Asp Ala Arg Lys Ala
245 250 255
Ile Ser Val Ala Glu Arg Gln Asn Tyr Ile Leu Gln Ile Arg Asp Leu
260 265 270
Ala Lys Gly Cys Ala Leu Leu Tyr Lys Glu Gln Glu Glu Glu Arg Glu
275 280 285
Glu Arg Leu Lys Asn Ala Leu Thr Lys Ala Glu Asn Gly Val Ser
290 295 300

<210> 105
<211> 1620
<212> DNA
<213> Helicobacter pylori
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<221> CDS
<222> (66)...(1538)

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Met Ala Gln Lys Thr Leu Leu Ile Ile Thr Asp Gly Ile Gly Tyr
1 5 10 15
cgt aaa gat agc gat cat aac gct ttc ttc cat gcc aaa aaa ccc act 158
Arg Lys Asp Ser Asp His Asn Ala Phe Phe His Ala Lys Lys Pro Thr
20 25 30
tat gat ttg atg ttt aaa acc ttg cct tat agc ctg att gat acg cat 206
Tyr Asp Leu Met Phe Lys Thr Leu Pro Tyr Ser Leu Ile Asp Thr His
35 40 45
ggc ttg agc gtg ggc tta cct aag ggg caa atg gga aat tct gaa gtg 254
Gly Leu Ser Val Gly Leu Pro Lys Gly Gln Met Gly Asn Ser Glu Val
50 55 60
ggg cat atg tgt att ggg gct ggt agg gtg ctc tat cag gat tta gtc 302
Gly His Met Cys Ile Gly Ala Gly Arg Val Leu Tyr Gln Asp Leu Val
65 70 75

aaa Lys 80	att Ile	tct Ser	tta Leu	agc Ser	ctt Leu 85	caa Gln	aac Asn	gat Asp	gaa Glu	tta Leu 90	aaa Lys	aac Asn	aac Asn	ccc Pro	gct Ala 95	350
ttt Phe	tta Leu	aac Asn	acg Thr	atc Ile 100	caa Gln	aaa Lys	agc Ser	cct Pro	gtg Val 105	gtg Val	cat His	ctt Leu	atg Met	ggt Gly 110	tta Leu	398
atg Met	agc Ser	gat Asp	gga Gly 115	ggc Gly	gtg Val	cat His	tca Ser	cac His	att Ile	gag Glu	cat His	ttt Phe	atc Ile 125	gct Ala	ctg Leu	446
gct Ala	tta Leu	gag Glu 130	tgt Cys	gaa Glu	aaa Lys	tcc Ser	cat His	aaa Lys 135	aaa Lys	gtc Val	tgt Cys	ctg Leu 140	cat His	tta Leu	atc Ile	494
acc Thr	gat Asp 145	ggg Gly	cgc Arg	gat Asp	gtc Val	gct Ala 150	cct Pro	aaa Lys	agc Ser	gct Ala	tta Leu 155	act Thr	tat Tyr	tta Leu	aaa Lys	542
caa Gln 160	atg Met	caa Gln	aat Asn	atc Ile	tgc Cys 165	aat Asn	gaa Glu	agc Ser	att Ile	caa Gln 170	atc Ile	gct Ala	acc Thr	ata Ile	agc Ser 175	590
ggc Gly	cgt Arg	ttt Phe	tat Tyr	gcc Ala 180	atg Met	gat Asp	agg Arg	gat Asp	aag Lys 185	cgc Arg	ttt Phe	gaa Glu	agg Arg	att Ile 190	gag Glu	638
ctt Leu	gcg Ala	tat Tyr	cat His 195	agc Ser	tta Leu	atg Met	ggg Gly	ctt Leu 200	aat Asn	cac His	acg Thr	cct Pro	tta Leu 205	agc Ser	cct Pro	686
agc Ser	gag Glu	tat Tyr 210	atc Ile	caa Gln	agc Ser	cag Gln	tat Tyr 215	gat Asp	aaa Lys	aat Asn	atc Ile	acc Thr 220	gat Asp	gaa Glu	ttt Phe	734
atc Ile	atg Met 225	ccc Pro	gct Ala	tgt Cys	ttt Phe	aaa Lys 230	aat Asn	tat Tyr	tgc Cys	ggc Gly	atg Met 235	caa Gln	gat Asp	gat Asp	gag Glu	782
agt Ser 240	ttt Phe	att Ile	ttt Phe	atc Ile	aat Asn 245	ttc Phe	agg Arg	aat Asn	gat Asp	agg Arg	gct Ala	aga Arg	gaa Glu	atc Ile	gtg Val 255	830
agc Ser	gct Ala	tta Leu	ggc Gly	caa Gln 260	aaa Lys	caa Gln	ttc Phe	agt Ser	ggc Gly 265	ttt Phe	aag Lys	cgc Arg	caa Gln	gtt Val 270	ttt Phe	878
aaa Lys	aaa Lys	ctc Leu	cat His 275	atc Ile	gct Ala	acc Thr	atg Met	acg Thr 280	cct Pro	tat Tyr	gat Asp	aac Asn	act Thr 285	ttc Phe	ccc Pro	926
tac Tyr	cct Pro	gtt Val 290	tta Leu	ttc Phe	ccc Pro	aaa Lys	gaa Glu 295	agc Ser	gtt Val	caa Gln	aac Asn	acg Thr 300	ctc Leu	gct Ala	gaa Glu	974
gtg Val	gtc Val	tct Ser	caa Gln	cac His	aac Asn	ctg Leu	acc Thr	caa Gln	agc Ser	cat His	atc Ile	gct Ala	gaa Glu	act Thr	gaa Glu	1022

305	310	315	
aaa tac gcg cat gta acc ttt ttc atc aat ggc gga gtg gag acg cct Lys Tyr Ala His Val Thr Phe Phe Ile Asn Gly Gly Val Glu Thr Pro 320 325 330 335			1070
ttt aaa aat gaa aac cgg gtg ctt atc caa agc cct aaa gtt acc act Phe Lys Asn Glu Asn Arg Val Leu Ile Gln Ser Pro Lys Val Thr Thr 340 345 350			1118
tat gac tta aag cct gaa atg agc gct aaa gaa gta acc ctt gcg gtg Tyr Asp Leu Lys Pro Glu Met Ser Ala Lys Glu Val Thr Leu Ala Val 355 360 365			1166
tta gag caa atg aaa cta ggc acg gat ttg atc att gtg aat ttt gct Leu Glu Gln Met Lys Leu Gly Thr Asp Leu Ile Ile Val Asn Phe Ala 370 375 380			1214
aat ggc gat atg gta ggg cat acg ggg aat ttt gaa gcg agc gtc aaa Asn Gly Asp Met Val Gly His Thr Gly Asn Phe Glu Ala Ser Val Lys 385 390 395			1262
gcg gtg gaa gca gtg gat gca tgt tta ggg gaa atc ctt tca ctg gct Ala Val Glu Ala Val Asp Ala Cys Leu Gly Glu Ile Leu Ser Leu Ala 400 405 410 415			1310
aaa aaa ttg gat tac gcc atg ctt tta acc agc gat cat ggg aat tgc Lys Lys Leu Asp Tyr Ala Met Leu Leu Thr Ser Asp His Gly Asn Cys 420 425 430			1358
gag cgc atg aaa gac gaa aac caa aac ccc tta acc aac cac acc gcc Glu Arg Met Lys Asp Glu Asn Gln Asn Pro Leu Thr Asn His Thr Ala 435 440 445			1406
ggg agc gtg tat tgc ttt gtt tta ggg gat gga gtc aaa tcc ata aaa Gly Ser Val Tyr Cys Phe Val Leu Gly Asp Gly Val Lys Ser Ile Lys 450 455 460			1454
aac gga gcc tta aac aat atc gct agc agc gtg tta aaa ctc atg ggc Asn Gly Ala Leu Asn Asn Ile Ala Ser Ser Val Leu Lys Leu Met Gly 465 470 475			1502
ctt aaa gcc cca gca acg atg gac gaa ccc cta ttt taaactaaag Leu Lys Ala Pro Ala Thr Met Asp Glu Pro Leu Phe 480 485 490			1548
gaaaagaatg caaattgatg acgcattatt gcaacgcttg gaaaaattga gcatgctaga gattaaagat ga			1608 1620
<210> 106			
<211> 491			
<212> PRT			
<213> Helicobacter pylori			
<400> 106			
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Lys Asp Ser Asp His Asn Ala Phe Phe His Ala Lys Lys Pro Thr Tyr 20 25 30			

00695913-062501

Asp	Leu	Met	Phe	Lys	Thr	Leu	Pro	Tyr	Ser	Leu	Ile	Asp	Thr	His	Gly
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Leu	Ser	Val	Gly	Leu	Pro	Lys	Gly	Gln	Met	Gly	Asn	Ser	Glu	Val	Gly
		50				55					60				
His	Met	Cys	Ile	Gly	Ala	Gly	Arg	Val	Leu	Tyr	Gln	Asp	Leu	Val	Lys
					70					75					80
Ile	Ser	Leu	Ser	Leu	Gln	Asn	Asp	Glu	Leu	Lys	Asn	Asn	Pro	Ala	Phe
				85					90					95	
Leu	Asn	Thr	Ile	Gln	Lys	Ser	Pro	Val	Val	His	Leu	Met	Gly	Leu	Met
			100					105					110		
Ser	Asp	Gly	Gly	Val	His	Ser	His	Ile	Glu	His	Phe	Ile	Ala	Leu	Ala
		115					120					125			
Leu	Glu	Cys	Glu	Lys	Ser	His	Lys	Lys	Val	Cys	Leu	His	Leu	Ile	Thr
		130				135					140				
Asp	Gly	Arg	Asp	Val	Ala	Pro	Lys	Ser	Ala	Leu	Thr	Tyr	Leu	Lys	Gln
					150					155					160
Met	Gln	Asn	Ile	Cys	Asn	Glu	Ser	Ile	Gln	Ile	Ala	Thr	Ile	Ser	Gly
				165					170					175	
Arg	Phe	Tyr	Ala	Met	Asp	Arg	Asp	Lys	Arg	Phe	Glu	Arg	Ile	Glu	Leu
			180					185					190		
Ala	Tyr	His	Ser	Leu	Met	Gly	Leu	Asn	His	Thr	Pro	Leu	Ser	Pro	Ser
		195					200					205			
Glu	Tyr	Ile	Gln	Ser	Gln	Tyr	Asp	Lys	Asn	Ile	Thr	Asp	Glu	Phe	Ile
		210				215					220				
Met	Pro	Ala	Cys	Phe	Lys	Asn	Tyr	Cys	Gly	Met	Gln	Asp	Asp	Glu	Ser
					230					235					240
Phe	Ile	Phe	Ile	Asn	Phe	Arg	Asn	Asp	Arg	Ala	Arg	Glu	Ile	Val	Ser
				245					250					255	
Ala	Leu	Gly	Gln	Lys	Gln	Phe	Ser	Gly	Phe	Lys	Arg	Gln	Val	Phe	Lys
			260					265					270		
Lys	Leu	His	Ile	Ala	Thr	Met	Thr	Pro	Tyr	Asp	Asn	Thr	Phe	Pro	Tyr
		275					280					285			
Pro	Val	Leu	Phe	Pro	Lys	Glu	Ser	Val	Gln	Asn	Thr	Leu	Ala	Glu	Val
						295					300				
Val	Ser	Gln	His	Asn	Leu	Thr	Gln	Ser	His	Ile	Ala	Glu	Thr	Glu	Lys
					310					315					320
Tyr	Ala	His	Val	Thr	Phe	Phe	Ile	Asn	Gly	Gly	Val	Glu	Thr	Pro	Phe
				325					330					335	
Lys	Asn	Glu	Asn	Arg	Val	Leu	Ile	Gln	Ser	Pro	Lys	Val	Thr	Thr	Tyr
			340					345					350		
Asp	Leu	Lys	Pro	Glu	Met	Ser	Ala	Lys	Glu	Val	Thr	Leu	Ala	Val	Leu
		355					360					365			
Glu	Gln	Met	Lys	Leu	Gly	Thr	Asp	Leu	Ile	Ile	Val	Asn	Phe	Ala	Asn
		370				375					380				
Gly	Asp	Met	Val	Gly	His	Thr	Gly	Asn	Phe	Glu	Ala	Ser	Val	Lys	Ala
					390					395					400
Val	Glu	Ala	Val	Asp	Ala	Cys	Leu	Gly	Glu	Ile	Leu	Ser	Leu	Ala	Lys
				405					410					415	
Lys	Leu	Asp	Tyr	Ala	Met	Leu	Leu	Thr	Ser	Asp	His	Gly	Asn	Cys	Glu
			420					425					430		
Arg	Met	Lys	Asp	Glu	Asn	Gln	Asn	Pro	Leu	Thr	Asn	His	Thr	Ala	Gly
		435					440					445			
Ser	Val	Tyr	Cys	Phe	Val	Leu	Gly	Asp	Gly	Val	Lys	Ser	Ile	Lys	Asn
		450				455					460				
Gly	Ala	Leu	Asn	Asn	Ile	Ala	Ser	Ser	Val	Leu	Lys	Leu	Met	Gly	Leu
					470					475					480
Lys	Ala	Pro	Ala	Thr	Met	Asp	Glu	Pro	Leu	Phe					
				485					490						

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 <211> 1440
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (72)...(1379)

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 gagtttttaa c atg aat ttt caa gaa aat tta gcc gct ttg gat ttg gag 110
 Met Asn Phe Gln Glu Asn Leu Ala Ala Leu Asp Leu Glu
 1 5 10

tat ctt tgg cac cct tgt tcg caa atg caa gag cat caa aat ttc ccc 158
 Tyr Leu Trp His Pro Cys Ser Gln Met Gln Glu His Gln Asn Phe Pro
 15 20 25

att atc ccc att aaa aag gct caa ggg att tac ctc tat gat ttt aat 206
 Ile Ile Pro Ile Lys Lys Ala Gln Gly Ile Tyr Leu Tyr Asp Phe Asn
 30 35 40 45

gat aac gct tac atg gat ttg atc agc tca tgg tgg gtg aat ctt ttt 254
 Asp Asn Ala Tyr Met Asp Leu Ile Ser Ser Trp Trp Val Asn Leu Phe
 50 55 60

ggg cat aat aac gcc tac atc agc cag caa ctc aaa aat caa att gat 302
 Gly His Asn Asn Ala Tyr Ile Ser Gln Gln Leu Lys Asn Gln Ile Asp
 65 70 75

gat tta gag cat gtc ctt ttg gct tct ttt agc cat aag ccc att atc 350
 Asp Leu Glu His Val Leu Leu Ala Ser Phe Ser His Lys Pro Ile Ile
 80 85 90

acg ctc tct caa agg ctt tgc cag ctc act cat atg gat aaa tgc ttt 398
 Thr Leu Ser Gln Arg Leu Cys Gln Leu Thr His Met Asp Lys Cys Phe
 95 100 105

tat gcg gat aac ggc tca tct tgt gtt gaa atc gct ttg aaa atg agc 446
 Tyr Ala Asp Asn Gly Ser Ser Cys Val Glu Ile Ala Leu Lys Met Ser
 110 115 120 125

tat cac gcc cat ttt tta aag aat caa acg cgc cgc aaa aag ctt ttt 494
 Tyr His Ala His Phe Leu Lys Asn Gln Thr Arg Arg Lys Lys Leu Phe
 130 135 140

tta tcg ctc tct aat tcc tat cat ggc gag act ttg gga gcg tta agc 542
 Leu Ser Leu Ser Asn Ser Tyr His Gly Glu Thr Leu Gly Ala Leu Ser
 145 150 155

gtg ggc gat gtg aaa ctt tat aaa gac act tac acc cct tta ttg ctc 590
 Val Gly Asp Val Lys Leu Tyr Lys Asp Thr Tyr Thr Pro Leu Leu Leu
 160 165 170

aaa aat ctc acc aca cct gtg cct aaa aac gac cat gaa ata gaa aat 638
 Lys Asn Leu Thr Thr Pro Val Pro Lys Asn Asp His Glu Ile Glu Asn
 175 180 185

006690-ET656860

agt Ser 190	ttg Leu	aac Asn	gct Ala	tta Leu	aag Lys 195	cgt Arg	ttg Leu	tta Leu	gac Asp	aag Lys 200	cat His	agt Ser	gaa Glu	gaa Glu	att Ile 205	686
tgc Cys	gct Ala	ttc Phe	att Ile	gca Ala 210	gag Glu	cct Pro	ctt Leu	ttg Leu	caa Gln 215	tgc Cys	gca Ala	ggg Gly	aat Asn	atg Met 220	cat His	734
att Ile	tat Tyr	agc Ser	gca Ala 225	aga Arg	tat Tyr	tta Leu	aaa Lys	caa Gln 230	gcc Ala	gtt Val	tta Leu	ttg Leu	tgc Cys 235	aag Lys	caa Gln	782
aaa Lys	aac Asn	atc Ile 240	cac His	att Ile	att Ile	ttt Phe	gat Asp 245	gaa Glu	atc Ile	gct Ala	acc Thr	ggg Gly 250	ttt Phe	ggg Gly	cgc Arg	830
aca Thr	ggg Gly 255	agc Ser	atg Met	ttt Phe	gct Ala	tat Tyr 260	gaa Glu	caa Gln	tgc Cys	gaa Glu	att Ile 265	aag Lys	ccg Pro	gat Asp	ttt Phe	878
tta Leu 270	tgc Cys	ttg Leu	tct Ser	aag Lys 275	ggg Gly	att Ile	agt Ser	ggg Gly	ggg Gly	tat Tyr 280	ttg Leu	cct Pro	tta Leu	agc Ser	gca Ala 285	926
cta Leu	tta Leu	acc Thr	cat His 290	aat Asn	gaa Glu	atc Ile	tat Tyr	aac Asn	caa Gln 295	ttt Phe	tac Tyr	gcc Ala	ccc Pro	tat Tyr 300	gaa Glu	974
gaa Glu	aat Asn	aaa Lys 305	gcg Ala	ttt Phe	ttg Leu	cat His	tcg Ser	cac His 310	agc Ser	tac Tyr	aca Thr	gga Gly	aac Asn 315	gct Ala	ttg Leu	1022
gca Ala	tgc Cys 320	gca Ala	tgc Cys	gcg Ala	aac Asn	gct Ala	acg Thr 325	ctg Leu	gat Asp	att Ile	ttt Phe	gaa Glu 330	aaa Lys	gaa Glu	aat Asn	1070
gtt Val	att Ile 335	gaa Glu	aag Lys	aac Asn	aag Lys	gct Ala 340	tta Leu	agc Ser	ggg Gly	ttt Phe 345	att Ile	ttt Phe	aat Asn	acg Thr	ctc Leu	1118
caa Gln 350	aac Asn	gca Ala	tta Leu	aaa Lys 355	ccc Pro	ttg Leu	atg Met	gag Glu	caa Gln 360	caa Gln	gtg Val	gtg Val	tct Ser	gat Asp	tta Leu 365	1166
agg Arg	cat His	ttg Leu	ggc Gly 370	atg Met	gtc Val	ttt Phe	gcc Ala	ttt Phe	gaa Glu 375	gtc Val	ttt Phe	att Ile	caa Gln	acc Thr 380	aaa Lys	1214
gag Glu	cgt Arg	ttg Leu 385	agt Ser	ttg Leu	gcg Ala	gtt Val	ttt Phe 390	aaa Lys	aaa Lys	act Thr	cta Leu	aaa Lys 395	aaa Lys	ggc Gly	ctg Leu	1262
tta Leu	tta Leu	cgc Arg 400	cct Pro	tta Leu	aac Asn	aac Asn	acc Thr 405	att Ile	tac Tyr	ctc Leu	atg Met 410	ccc Pro	cct Pro	tac Tyr	att Ile	1310
atc Ile	acg Thr 415	cat His	gaa Glu	gaa Glu	gtc Val	aaa Lys 420	aag Lys	gcg Ala	gtt Val	gcg Ala	ggg Gly 425	cta Leu	gtg Val	gaa Glu	att Ile	1358

Gly Met Val Phe Ala Phe Glu Val Phe Ile Gln Thr Lys Glu Arg Leu
 370 375 380
 Ser Leu Ala Val Phe Lys Lys Thr Leu Lys Lys Gly Leu Leu Leu Arg
 385 390 395 400
 Pro Leu Asn Asn Thr Ile Tyr Leu Met Pro Tyr Ile Ile Thr His
 405 410 415
 Glu Glu Val Lys Lys Ala Val Ala Gly Leu Val Glu Ile Leu Asp Glu
 420 425 430
 Leu Arg Lys Gly
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 <213> Helicobacter pylori

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 Met Gly Lys Met Lys Gln Glu Thr Ala Ile
 1 5 10
 gac tat gaa aaa tta gcg aat cat tgg aat aat aat gat gaa aac agc 159
 Asp Tyr Glu Lys Leu Ala Asn His Trp Asn Asn Asn Asp Glu Asn Ser
 15 20 25
 gaa gca cta aac gct ttt gca gac gct tac ctt tat aaa cat gag aaa 207
 Glu Ala Leu Asn Ala Phe Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys
 30 35 40
 aag agt caa aag att cgg gca ata gag ata agt tct cta aac aaa gcc 255
 Lys Ser Gln Lys Ile Arg Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala
 45 50 55
 tgc atg gga gaa ttt tac cac aaa aac cca aaa tta ttt taataacgat 304
 Cys Met Gly Glu Phe Tyr His Lys Asn Pro Lys Leu Phe
 60 65 70
 cgctccaagg aaccaacgcc ccatgacctc aagaaaagag aatagcttga atcggt 360

<210> 110
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 <212> PRT
 <213> Helicobacter pylori

<400> 110
 Met Gly Lys Met Lys Gln Glu Thr Ala Ile Asp Tyr Glu Lys Leu Ala
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 Asn His Trp Asn Asn Asn Asp Glu Asn Ser Glu Ala Leu Asn Ala Phe
 20 25 30
 Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys Lys Ser Gln Lys Ile Arg
 35 40 45
 Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala Cys Met Gly Glu Phe Tyr
 50 55 60
 His Lys Asn Pro Lys Leu Phe

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<220>
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 <222> (62)...(1255)

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 a aga cat aga aac aga gct aga tgc act aga aaa cag gct aga aac aat 109
 Arg His Arg Asn Arg Ala Arg Cys Thr Arg Lys Gln Ala Arg Asn Asn
 1 5 10 15

aag agt ttt agg cat gaa aac tat ttt tat aaa gtt ttg ggt agt gca 157
 Lys Ser Phe Arg His Glu Asn Tyr Phe Tyr Lys Val Leu Gly Ser Ala
 20 25 30

act tct caa ata gaa agt ttg aaa aaa aga gaa aat gcc cta ttt gat 205
 Thr Ser Gln Ile Glu Ser Leu Lys Lys Arg Glu Asn Ala Leu Phe Asp
 35 40 45

cat tta gat agt cta aaa agt tta tta gaa aaa aca cat tgg gaa aaa 253
 His Leu Asp Ser Leu Lys Ser Leu Leu Glu Lys Thr His Trp Glu Lys
 50 55 60

gaa aaa ttc acg ccc cca ata aat gaa aaa gaa ctt aat agg caa ctt 301
 Glu Lys Phe Thr Pro Ile Asn Glu Lys Glu Leu Asn Arg Gln Leu
 65 70 75 80

aaa gaa gtg aga tgg ttc aat aaa gaa act cca act tct aaa aac act 349
 Lys Glu Val Arg Trp Phe Asn Lys Glu Thr Pro Thr Ser Lys Asn Thr
 85 90 95

tat aag aaa att caa aaa tta gct gtt tat aaa agc cct tta ata aaa 397
 Tyr Lys Lys Ile Gln Lys Leu Ala Val Tyr Lys Ser Pro Leu Ile Lys
 100 105 110

gat tat ctt tat acc att aaa aaa ctt ttt gcc aca caa aaa aag att 445
 Asp Tyr Leu Tyr Thr Ile Lys Lys Leu Phe Ala Thr Gln Lys Lys Ile
 115 120 125

ata gat tta gaa aaa aat tat aaa gat tta aga gcc tta aag gaa gaa 493
 Ile Asp Leu Glu Lys Asn Tyr Lys Asp Leu Arg Ala Leu Lys Glu Glu
 130 135 140

ttt agc aaa gat tta gaa act gat tta tcc cat tca aaa aaa cgc ttt 541
 Phe Ser Lys Asp Leu Glu Thr Asp Leu Ser His Ser Lys Lys Arg Phe
 145 150 155 160

gaa ctt tac act aga cta aag agc atg agc aaa gtt ttt ata agc aaa 589
 Glu Leu Tyr Thr Arg Leu Lys Ser Met Ser Lys Val Phe Ile Ser Lys
 165 170 175

agc att gtt aaa aat tta gaa aaa att gct tta gat ttt aaa agc gat 637
 Ser Ile Val Lys Asn Leu Glu Lys Ile Ala Leu Asp Phe Lys Ser Asp

180						185						190						
aga	cat	agt	att	tcg	caa	aga	gct	ttt	gaa	ttt	ttt	aag	tat	atg	aat	685		
Arg	His	Ser	Ile	Ser	Gln	Arg	Ala	Phe	Glu	Phe	Phe	Lys	Tyr	Met	Asn			
195						200						205						
tat	caa	aat	tta	agc	ttg	act	gat	aaa	ggc	aat	atg	ttt	tta	gtg	gct	733		
Tyr	Gln	Asn	Leu	Ser	Leu	Thr	Asp	Lys	Gly	Asn	Met	Phe	Leu	Val	Ala			
210						215						220						
aag	ttt	ttt	aaa	gat	agt	gct	tta	ctt	gtt	aat	att	gct	agg	ttt	gaa	781		
Lys	Phe	Phe	Lys	Asp	Ser	Ala	Leu	Leu	Val	Asn	Ile	Ala	Arg	Phe	Glu			
225						230						235						
atg	aaa	aag	ata	gat	gat	agt	gtt	aaa	aat	tct	aac	cca	caa	gac	aat	829		
Met	Lys	Lys	Ile	Asp	Asp	Ser	Val	Lys	Asn	Ser	Asn	Pro	Gln	Asp	Asn			
245						250						255						
tta	tta	gac	aaa	caa	gtt	tgg	ctc	aat	ctt	tta	gag	cat	tta	aaa	aga	877		
Leu	Leu	Asp	Lys	Gln	Val	Trp	Leu	Asn	Leu	Leu	Glu	His	Leu	Lys	Arg			
260						265						270						
ctt	gaa	gag	gaa	aat	tat	tgt	ttt	gct	aag	aaa	cga	aaa	gaa	ttc	tta	925		
Leu	Glu	Glu	Glu	Asn	Tyr	Cys	Phe	Ala	Lys	Lys	Arg	Lys	Glu	Phe	Leu			
275						280						285						
gag	act	aga	gcg	atg	gag	cta	tca	aaa	gat	tta	aaa	ttt	tta	aca	cag	973		
Glu	Thr	Arg	Ala	Met	Glu	Leu	Ser	Lys	Asp	Leu	Lys	Phe	Leu	Thr	Gln			
290						295						300						
gct	aat	gaa	aat	gat	ttg	ccc	att	tat	gaa	aga	ggg	caa	agg	gat	aaa	1021		
Ala	Asn	Glu	Asn	Asp	Leu	Pro	Ile	Tyr	Glu	Arg	Gly	Gln	Arg	Asp	Lys			
305						310						315						
atc	att	aaa	cgc	tgt	gaa	aaa	tcg	ctt	aac	ttt	ttg	cag	aaa	gaa	tta	1069		
Ile	Ile	Lys	Arg	Cys	Glu	Lys	Ser	Leu	Asn	Phe	Leu	Gln	Lys	Glu	Leu			
325						330						335						
caa	tgc	ttt	aaa	acc	tta	ttg	aaa	agt	gca	agt	ata	gct	tta	gaa	aac	1117		
Gln	Cys	Phe	Lys	Thr	Leu	Leu	Lys	Ser	Ala	Ser	Ile	Ala	Leu	Glu	Asn			
340						345						350						
ttg	caa	aat	aac	cat	caa	atc	aca	gcc	gtt	aca	caa	gac	acg	caa	gaa	1165		
Leu	Gln	Asn	Asn	His	Gln	Ile	Thr	Ala	Val	Thr	Gln	Asp	Thr	Gln	Glu			
355						360						365						
aac	aca	aac	gcg	ctc	aaa	aat	act	act	caa	gat	ttt	aac	aaa	act	acc	1213		
Asn	Thr	Asn	Ala	Leu	Lys	Asn	Thr	Thr	Gln	Asp	Phe	Asn	Lys	Thr	Thr			
370						375						380						
aat	gaa	cca	aca	aac	cct	aac	aat	aac	tat	gga	atg	gat	ttt			1255		
Asn	Glu	Pro	Thr	Asn	Pro	Asn	Asn	Asn	Tyr	Gly	Met	Asp	Phe					
385						390						395						
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06997

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Lys	Ser	Phe	Arg 20	His	Glu	Asn	Tyr	Phe 25	Tyr	Lys	Val	Leu	Gly 30	Ser	Ala
Thr	Ser	Gln 35	Ile	Glu	Ser	Leu	Lys 40	Lys	Arg	Glu	Asn	Ala 45	Leu	Phe	Asp
His	Leu 50	Asp	Ser	Leu	Lys	Ser 55	Leu	Leu	Glu	Lys	Thr 60	His	Trp	Glu	Lys
Glu 65	Lys	Phe	Thr	Pro	Pro 70	Ile	Asn	Glu	Lys	Glu 75	Leu	Asn	Arg	Gln	Leu 80
Lys	Glu	Val	Arg 85	Trp	Phe	Asn	Lys	Glu	Thr 90	Pro	Thr	Ser	Lys	Asn 95	Thr
Tyr	Lys	Lys	Ile 100	Gln	Lys	Leu	Ala	Val 105	Tyr	Lys	Ser	Pro	Leu	Ile	Lys
Asp	Tyr	Leu 115	Tyr	Thr	Ile	Lys	Lys 120	Leu	Phe	Ala	Thr	Gln 125	Lys	Lys	Ile
Ile	Asp 130	Leu	Glu	Lys	Asn	Tyr 135	Lys	Asp	Leu	Arg	Ala 140	Leu	Lys	Glu	Glu
Phe 145	Ser	Lys	Asp	Leu	Glu 150	Thr	Asp	Leu	Ser	His 155	Ser	Lys	Lys	Arg	Phe 160
Glu	Leu	Tyr	Thr 165	Arg	Leu	Lys	Ser	Met	Ser 170	Lys	Val	Phe	Ile	Ser 175	Lys
Ser	Ile	Val 180	Lys	Asn	Leu	Glu	Lys	Ile 185	Ala	Leu	Asp	Phe 190	Lys	Ser	Asp
Arg	His	Ser 195	Ile	Ser	Gln	Arg	Ala 200	Phe	Glu	Phe	Phe 205	Lys	Tyr	Met	Asn
Tyr	Gln 210	Asn	Leu	Ser	Leu	Thr 215	Asp	Lys	Gly	Asn	Met 220	Phe	Leu	Val	Ala
Lys 225	Phe	Phe	Lys	Asp	Ser 230	Ala	Leu	Leu	Val	Asn 235	Ile	Ala	Arg	Phe	Glu 240
Met	Lys	Lys	Ile 245	Asp	Asp	Ser	Val	Lys	Asn 250	Ser	Asn	Pro	Gln	Asp 255	Asn
Leu	Leu	Asp	Lys 260	Gln	Val	Trp	Leu	Asn 265	Leu	Leu	Glu	His 270	Leu	Lys	Arg
Leu	Glu	Glu 275	Glu	Asn	Tyr	Cys	Phe 280	Ala	Lys	Lys	Arg	Lys 285	Glu	Phe	Leu
Glu	Thr 290	Arg	Ala	Met	Glu	Leu 295	Ser	Lys	Asp	Leu	Lys 300	Phe	Leu	Thr	Gln
Ala 305	Asn	Glu	Asn	Asp	Leu 310	Pro	Ile	Tyr	Glu	Arg 315	Gly	Gln	Arg	Asp	Lys
Ile	Ile	Lys	Arg 325	Cys	Glu	Lys	Ser	Leu	Asn 330	Phe	Leu	Gln	Lys	Glu 335	Leu
Gln	Cys	Phe	Lys 340	Thr	Leu	Leu	Lys	Ser 345	Ala	Ser	Ile	Ala 350	Leu	Glu	Asn
Leu	Gln 355	Asn	Asn	His	Gln	Ile	Thr 360	Ala	Val	Thr	Gln	Asp 365	Thr	Gln	Glu
Asn	Thr 370	Asn	Ala	Leu	Lys	Asn 375	Thr	Thr	Gln	Asp	Phe 380	Asn	Lys	Thr	Thr
Asn 385	Glu	Pro	Thr	Asn 390	Pro	Asn	Asn	Asn	Tyr	Gly 395	Met	Asp	Phe		

<213> Helicobacter pylori

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<210> 114
<211> 138
<212> PRT
<213> Helicobacter pylori
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-125-

SECRET

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-126-

[illegible]

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			20					25					30			

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caa agc cct ttt gtg agc gtt tta gaa cgc att aat ttg ccc ttt att Gln Ser Pro Phe Val Ser Val Leu Glu Arg Ile Asn Leu Pro Phe Ile 320 325 330	1069
ggc atg ggt atc cct tat gtg gct gat ata atg aac gct gtt atc att Gly Met Gly Ile Pro Tyr Val Ala Asp Ile Met Asn Ala Val Ile Ile 335 340 345 350	1117
acg gcg atg ttt tct acc gct aat tca ggg ctt tat gga gcg agc cgc Thr Ala Met Phe Ser Thr Ala Asn Ser Gly Leu Tyr Gly Ala Ser Arg 355 360 365	1165
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caa ctc aac cga caa ggc acg ccc act tat gcg atg ttt ttt tcc ctt Gln Leu Asn Arg Gln Gly Thr Pro Thr Tyr Ala Met Phe Phe Ser Leu 385 390 395	1261
tct ttt tct ctc ata ggg ctt tta gtc caa att tat gcc aaa gaa aat Ser Phe Ser Leu Ile Gly Leu Leu Val Gln Ile Tyr Ala Lys Glu Asn 400 405 410	1309
gtc gtg gaa gct ttg att aat gtg atc agt ttc acg gtg att att gtg Val Val Glu Ala Leu Ile Asn Val Ile Ser Phe Thr Val Ile Ile Val 415 420 425 430	1357
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aaa gcc ggg cat tct tta gag gat ttg cct tat aaa gcc ccc ttt cta Lys Ala Gly His Ser Leu Glu Asp Leu Pro Tyr Lys Ala Pro Phe Leu 450 455 460	1453
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ggt tcg gct atg gat aag gat caa cgc att ggg atg att tta acg att Gly Ser Ala Met Asp Lys Asp Gln Arg Ile Gly Met Ile Leu Thr Ile 480 485 490	1549
gtt ttc gct gtt att tgt tac att gga tac tat ttt aca caa aaa gct Val Phe Ala Val Ile Cys Tyr Ile Gly Tyr Tyr Phe Thr Gln Lys Ala 495 500 505 510	1597
aat gaa aat aac aaa aaa gat ttg ata taatcttttc ttaattttga Asn Glu Asn Asn Lys Lys Asp Leu Ile 515	1644

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1704
1709

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<211> 519
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<213> Helicobacter pylori

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Lys Lys Ser Phe Tyr Phe Ile Phe Val Ile Ile Gln Ala Ile Phe Ile
20 25 30
Phe Asn Leu Arg Arg Cys Arg Met Asp Asn Gln Lys Ile Thr His Gln
35 40 45
Asn Ile Thr Gln Lys Gln Gly Glu Leu Lys Arg Asp Met Lys Met Arg
50 55 60
His Leu Leu Met Ile Ala Phe Gly Gly Ala Ile Gly Thr Gly Leu Phe
65 70 75 80
Val Gly Thr Gly Gly Asn Ile Ala Ser Ala Gly Pro Leu Gly Thr Leu
85 90 95
Ile Ala Tyr Cys Phe Gly Gly Leu Val Val Tyr Cys Ile Met Leu Ser
100 105 110
Leu Gly Glu Leu Ala Ser Val Tyr Pro Thr Thr Gly Ser Phe Gly Asp
115 120 125
Tyr Ala Ala Lys Phe Ile Gly Pro Gly Thr Gly Tyr Met Val Phe Trp
130 135 140
Met Tyr Trp Leu Gly Trp Val Ile Thr Val Ala Leu Glu Tyr Ile Ala
145 150 155 160
Ile Gly Met Leu Met Gln Arg Trp Phe Ala Asp Ile Pro Ile His Tyr
165 170 175
Trp Val Ile Leu Cys Ile Ala Leu Val Phe Leu Leu Asn Phe Phe Ser
180 185 190
Val Lys Ile Phe Ala Glu Gly Glu Phe Phe Phe Ser Leu Ile Lys Val
195 200 205
Leu Ala Val Ile Ala Phe Ile Gly Ile Gly Ala Ile Gly Ile Ile Tyr
210 215 220
Gln Ile Tyr Ser His Gly Phe Gly Ser Ile Phe Asp Asn Phe His Phe
225 230 235 240
Gly Asp Lys Gly Phe Phe Pro Asn Gly Ser Ala Ala Val Phe Ser Ala
245 250 255
Met Leu Ala Val Ile Phe Ala Phe Thr Gly Thr Glu Val Ile Gly Val
260 265 270
Ala Val Gly Glu Thr Lys Asn Ala Ser Glu Val Met Pro Lys Ala Ile
275 280 285
Lys Ala Thr Leu Trp Arg Ile Val Phe Phe Phe Leu Gly Ser Val Phe
290 295 300
Val Ile Ser Val Phe Leu Pro Met Asn Asp Ser Ser Ile Thr Gln Ser
305 310 315 320
Pro Phe Val Ser Val Leu Glu Arg Ile Asn Leu Pro Phe Ile Gly Met
325 330 335
Gly Ile Pro Tyr Val Ala Asp Ile Met Asn Ala Val Ile Ile Thr Ala
340 345 350
Met Phe Ser Thr Ala Asn Ser Gly Leu Tyr Gly Ala Ser Arg Met Ile
355 360 365
Tyr Gly Leu Ser Lys Gln Lys Met Phe Phe Lys Val Phe Ser Gln Leu
370 375 380
Asn Arg Gln Gly Thr Pro Thr Tyr Ala Met Phe Phe Ser Leu Ser Phe

09095913.062901

caa ggt aac att atc aca aaa att gaa gag gtt gaa gtt aaa agc gtt	1294
Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val Lys Ser Val	
340 345 350 355	
gcg gat ttt aac cat gct tta gaa aag tat aaa ggc aaa ccc aaa cga	1342
Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys Pro Lys Arg	
360 365 370	
ttc tta gtt tta gac ttg aat caa ggt tat agg atc att ttg gtg aaa	1390
Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile Leu Val Lys	
375 380 385	
tgataggggt gggtcgtag tcgcatgtct ttgattagag tgaatgggga agctttttaa	1450
ctctcttttag aaagttaga agaagaccct ttgaaacta aagaaacgct agaaacgctt	1510
atcaaacaaa cgagcgttg	1529

<210> 120
 <211> 387
 <212> PRT
 <213> Helicobacter pylori

<400> 120	
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1 5 10 15	
Ile Ser Lys Asp Gly Tyr Ile Val Thr Asn Asn His Val Ile Asp Gly	
20 25 30	
Ala Asp Lys Ile Lys Val Thr Ile Pro Gly Ser Asn Lys Glu Tyr Ser	
35 40 45	
Ala Thr Leu Val Gly Thr Asp Ser Glu Ser Asp Leu Ala Val Ile Arg	
50 55 60	
Ile Thr Lys Asp Asn Leu Pro Thr Ile Lys Phe Ser Asp Ser Asn Asp	
65 70 75 80	
Ile Ser Val Gly Asp Leu Val Phe Ala Ile Gly Asn Pro Phe Gly Val	
85 90 95	
Gly Glu Ser Val Thr Gln Gly Ile Val Ser Ala Leu Asn Lys Ser Gly	
100 105 110	
Ile Gly Ile Asn Ser Tyr Glu Asn Phe Ile Gln Thr Asp Ala Ser Ile	
115 120 125	
Asn Pro Gly Asn Ser Gly Gly Ala Leu Ile Asp Ser Arg Gly Gly Leu	
130 135 140	
Val Gly Ile Asn Thr Ala Ile Ile Ser Lys Thr Gly Gly Asn His Gly	
145 150 155 160	
Ile Gly Phe Ala Ile Pro Ser Asn Met Val Lys Asp Thr Val Thr Gln	
165 170 175	
Leu Ile Lys Thr Gly Lys Ile Glu Arg Gly Tyr Leu Gly Val Gly Leu	
180 185 190	
Gln Asp Leu Ser Gly Asp Leu Gln Asn Ser Tyr Asp Asn Lys Glu Gly	
195 200 205	
Ala Val Val Ile Ser Val Glu Lys Asp Ser Pro Ala Lys Lys Ala Gly	
210 215 220	
Ile Leu Val Trp Asp Leu Ile Thr Glu Val Asn Gly Lys Lys Val Lys	
225 230 235 240	
Asn Thr Asn Glu Leu Arg Asn Leu Ile Gly Ser Met Leu Pro Asn Gln	
245 250 255	
Arg Val Thr Leu Lys Val Ile Arg Asp Lys Lys Glu Arg Ala Phe Thr	
260 265 270	
Leu Thr Leu Ala Glu Arg Lys Asn Pro Asn Lys Lys Glu Thr Ile Ser	
275 280 285	

Ala Gln Asn Gly Ala Gln Gly Gln Leu Asn Gly Leu Gln Val Glu Asp
 290 295 300
 Leu Thr Gln Glu Thr Lys Arg Ser Met Arg Leu Ser Asp Asp Val Gln
 305 310 315 320
 Gly Val Leu Val Ser Gln Val Asn Glu Asn Ser Pro Ala Glu Gln Ala
 325 330 335
 Gly Phe Arg Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val
 340 345 350
 Lys Ser Val Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys
 355 360 365
 Pro Lys Arg Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile
 370 375 380
 Leu Val Lys
 385

<210> 121
 <211> 990
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (39)...(902)

<400> 121
 atgatagtat tctaataaaa ctatttttaaa ggtgatcc atg agt aag agt tta tac 56
 Met Ser Lys Ser Leu Tyr
 1 5
 caa act tta aat gtg agc gaa aac gcc agc caa gat gaa atc aaa aaa 104
 Gln Thr Leu Asn Val Ser Glu Asn Ala Ser Gln Asp Glu Ile Lys Lys
 10 15 20
 tcc tac cgc cgt tta gcc cga caa tac cac ccg gat ttg aat aaa acc 152
 Ser Tyr Arg Arg Leu Ala Arg Gln Tyr His Pro Asp Leu Asn Lys Thr
 25 30 35
 aaa gaa gcc gaa gag aaa ttc aaa gaa atc aac gcc gct tat gaa att 200
 Lys Glu Ala Glu Glu Lys Phe Lys Glu Ile Asn Ala Ala Tyr Glu Ile
 40 45 50
 ttg agc gat gaa gaa aaa cgc cgc caa tac gat cag ttt ggc gat aac 248
 Leu Ser Asp Glu Glu Lys Arg Arg Gln Tyr Asp Gln Phe Gly Asp Asn
 55 60 65 70
 atg ttt ggc ggg cag aat ttc agc gat ttt gcc aga agc cgt ggt cct 296
 Met Phe Gly Gly Gln Asn Phe Ser Asp Phe Ala Arg Ser Arg Gly Pro
 75 80 85
 agt gaa gat tta gac gat att tta agc tct att ttt ggg aaa gga ggc 344
 Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser Ile Phe Gly Lys Gly Gly
 90 95 100
 ttt tcg caa aga ttt tct caa aac tcg caa ggc ttt tct ggc ttt aat 392
 Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln Gly Phe Ser Gly Phe Asn
 105 110 115
 ttt tcc aat ttc gcc cct gaa aat tta gac ata acc gcc gct tta aat 440
 Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp Ile Thr Ala Ala Leu Asn

Asp Gln Phe Gly Asp Asn Met Phe Gly Gly Gln Asn Phe Ser Asp Phe
65 70 75 80
Ala Arg Ser Arg Gly Pro Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser
85 90 95
Ile Phe Gly Lys Gly Gly Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln
100 105 110
Gly Phe Ser Gly Phe Asn Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp
115 120 125
Ile Thr Ala Ala Leu Asn Val Ser Val Leu Asp Thr Leu Leu Gly Asn
130 135 140
Lys Lys Gln Val Ser Ile Asn Asn Glu Thr Phe Ser Leu Lys Ile Pro
145 150 155 160
Ile Gly Val Glu Glu Gly Glu Lys Ile Arg Val Arg Asn Lys Gly Lys
165 170 175
Thr Gly Arg Thr Thr Arg Gly Asp Leu Leu Leu Glu Ile His Ile Glu
180 185 190
Glu Asp Glu Met Tyr Arg Arg Glu Lys Asp Asp Ile Thr Gln Ile Phe
195 200 205
Asp Leu Pro Leu Lys Thr Ala Leu Phe Gly Gly Lys Ile Glu Ile Ala
210 215 220
Thr Trp His Lys Thr Leu Thr Leu Thr Ile Pro Pro Asn Thr Lys Ala
225 230 235 240
Met Gln Lys Phe Arg Ile Lys Glu Lys Gly Ile Lys Asn Arg Lys Thr
245 250 255
Ser His Val Gly Asp Leu Tyr Leu Gln Ala Arg Leu Ile Leu Pro Lys
260 265 270
Thr Glu Thr Leu Ser Asn Glu Leu Lys Ala Leu Leu Glu Lys Glu Leu
275 280 285

<210> 123
<211> 1350
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (113)...(1285)

<400> 123
acctgaataa agagttgcaa gacgctctgc acaaacactc taaaaatacc aaaaccccaa 60
cgaaaaattt aaacaccctt acgaattttt acgaattgat tttattttaa aa atg agc 118
Met Ser
1
ctg act tcg ctt tta aac cca aaa agc cta gaa gat ttt tta ggc caa 166
Leu Thr Ser Leu Leu Asn Pro Lys Ser Leu Glu Asp Phe Leu Gly Gln
5 10 15
gag cat tta gta ggg aaa gac gcc ccc tta ttt aaa gcc cta caa tcc 214
Glu His Leu Val Gly Lys Asp Ala Pro Leu Phe Lys Ala Leu Gln Ser
20 25 30
aaa cac ttc ccc cat gcc ttt ttc tat ggc cct cct ggc gtg ggt aaa 262
Lys His Phe Pro His Ala Phe Phe Tyr Gly Pro Pro Gly Val Gly Lys
35 40 45 50
aca agc ctg gct caa atc atc gcc tat atg cta gag cgc ccc att ctt 310
Thr Ser Leu Ala Gln Ile Ile Ala Tyr Met Leu Glu Arg Pro Ile Leu
55 60 65

tta ttc aat gcg acg gat ttt aaa tta gag gat ttg cgc ctt aag ctt	358
Leu Phe Asn Ala Thr Asp Phe Lys Leu Glu Asp Leu Arg Leu Lys Leu	
70 75 80	
aaa aat tac caa aat acc ctt tta aaa ccc gtt gtt ttt att gat gaa	406
Lys Asn Tyr Gln Asn Thr Leu Leu Lys Pro Val Val Phe Ile Asp Glu	
85 90 95	
acc cac aga ttg aat aaa acc caa caa gaa ttt tta ctc ccc att atg	454
Thr His Arg Leu Asn Lys Thr Gln Gln Glu Phe Leu Leu Pro Ile Met	
100 105 110	
gaa aaa gat cac gct tta att tta ggg gct agc acg caa gat cct aat	502
Glu Lys Asp His Ala Leu Ile Leu Gly Ala Ser Thr Gln Asp Pro Asn	
115 120 125 130	
tac agc cta agc cat gcg atc cga tca aga agt ttt att ttt gaa tta	550
Tyr Ser Leu Ser His Ala Ile Arg Ser Arg Ser Phe Ile Phe Glu Leu	
135 140 145	
acc ccc cta aac aag agc gat tta gac agg ctt tgc gct aaa gct tta	598
Thr Pro Leu Asn Lys Ser Asp Leu Asp Arg Leu Cys Ala Lys Ala Leu	
150 155 160	
aca ttg ctc aaa aaa caa ata gag cct ggc gct aaa acc tat ctt tta	646
Thr Leu Leu Lys Lys Gln Ile Glu Pro Gly Ala Lys Thr Tyr Leu Leu	
165 170 175	
aac aac agc gct ggc gac gct aga gcg tta tta aac ctt tta gat ttg	694
Asn Asn Ser Ala Gly Asp Ala Arg Ala Leu Leu Asn Leu Leu Asp Leu	
180 185 190	
agc gct aaa ata gaa gat cct atc act tta aaa acg cta caa tcc tta	742
Ser Ala Lys Ile Glu Asp Pro Ile Thr Leu Lys Thr Leu Gln Ser Leu	
195 200 205 210	
cgg cct cat agc cta aat gat gga tct tat agc gat gat acg cat tat	790
Arg Pro His Ser Leu Asn Asp Gly Ser Tyr Ser Asp Asp Thr His Tyr	
215 220 225	
aac ctt act agc gcg tta atc aaa tct tta aga ggg agc gat gaa aac	838
Asn Leu Thr Ser Ala Leu Ile Lys Ser Leu Arg Gly Ser Asp Glu Asn	
230 235 240	
gct tcc atc tat tat ctg gcg cgc ttg att gct ggc ggg gaa aac ccg	886
Ala Ser Ile Tyr Tyr Leu Ala Arg Leu Ile Ala Gly Gly Glu Asn Pro	
245 250 255	
gaa ttt atc gcc aga agg ctg gtg att ttt gcg agc gaa gat att ggt	934
Glu Phe Ile Ala Arg Arg Leu Val Ile Phe Ala Ser Glu Asp Ile Gly	
260 265 270	
aac gct aac ccg aac gcc ctt aat tta gcc gct tct tgt ttg ttt gca	982
Asn Ala Asn Pro Asn Ala Leu Asn Leu Ala Ala Ser Cys Leu Phe Ala	
275 280 285 290	
gtc aaa caa atc ggc tac cct gaa gcg cgc atc att tta agc caa tgc	1030
Val Lys Gln Ile Gly Tyr Pro Glu Ala Arg Ile Ile Leu Ser Gln Cys	

195	200	205
Ser Leu Arg Pro His Ser	Leu Asn Asp Gly Ser Tyr	Ser Asp Asp Thr
210	215	220
His Tyr Asn Leu Thr Ser	Ala Leu Ile Lys Ser	Leu Arg Gly Ser Asp
225	230	235
Glu Asn Ala Ser Ile Tyr	Tyr Leu Ala Arg Leu	Ile Ala Gly Gly Glu
245	250	255
Asn Pro Glu Phe Ile Ala	Arg Arg Leu Val Ile Phe	Ala Ser Glu Asp
260	265	270
Ile Gly Asn Ala Asn Pro	Asn Ala Leu Asn Leu	Ala Ala Ser Cys Leu
275	280	285
Phe Ala Val Lys Gln Ile	Gly Tyr Pro Glu Ala	Arg Ile Ile Leu Ser
290	295	300
Gln Cys Val Ile Tyr Leu	Ala Cys Ser Pro Lys	Ser Asn Thr Ala Tyr
305	310	315
Arg Ala Ile Asn Gln Ala	Leu Asp Cys Val Gln	Lys Gly Ser Leu Tyr
325	330	335
Pro Ile Pro Lys His Leu	Leu Pro Asn Ala Lys	Asp Tyr Leu Tyr Pro
340	345	350
His Asp Tyr Asn Gly Tyr	Val Lys Gln Asp Tyr	Leu Glu Lys Pro Leu
355	360	365
Asp Leu Val Ser Ser Gln	Gly Ile Gly Phe Glu	Lys Thr Leu Leu Glu
370	375	380
Trp Leu Asp Lys Ile Arg	Asn	
385	390	

<210> 125
 <211> 869
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (76)...(759)

<400> 125	
aagaaacttt taacaaacaa ttcaagggat ttggcgattt tgggtcttaa aaaatatgct	60
attttatggt cttta atg ggg ttt tat gca gga ttg aac gcg ctt gat tat	111
Met Gly Phe Tyr Ala Gly Leu Asn Ala Leu Asp Tyr	
1 5 10	
gac acc ata gac cca aaa tac tac aag tat atc aag tat tat aaa gcc	159
Asp Thr Ile Asp Pro Lys Tyr Tyr Lys Tyr Ile Lys Tyr Tyr Lys Ala	
15 20 25	
tat gag gat aaa gaa gtt gaa gaa ttg atc aga gac tta aaa agg gcg	207
Tyr Glu Asp Lys Glu Val Glu Glu Leu Ile Arg Asp Leu Lys Arg Ala	
30 35 40	
aac gct aaa agc ggg ctt att tta ggg atc aat acc ggg ttt ttt tac	255
Asn Ala Lys Ser Gly Leu Ile Leu Gly Ile Asn Thr Gly Phe Phe Tyr	
45 50 55 60	
aat cat gaa atc atg gtt aga act aat agc tct agc atc acg ggg aat	303
Asn His Glu Ile Met Val Arg Thr Asn Ser Ser Ser Ile Thr Gly Asn	
65 70 75	
att tta aat tat ttg ttc gct tac ggc ttg cgt ttt ggc tat caa act	351
Ile Leu Asn Tyr Leu Phe Ala Tyr Gly Leu Arg Phe Gly Tyr Gln Thr	

80	85	90	
ttc agg ccg tcg ttt ttt gcg cgc ttg gtc aag cca aat atc att ggc			399
Phe Arg Pro Ser Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly			
95	100	105	
agg cgc att tat atc caa tat tat gga gga gct cct aaa aaa gcg ggc			447
Arg Arg Ile Tyr Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly			
110	115	120	
ttt ggg gat gta ggg ttt caa tcg gtt atg ctg aat ggg gat ttt tta			495
Phe Gly Asp Val Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu			
125	130	135	140
ttg gat ttt cct ttg cct ttt gtg ggg aaa tac ctt tat atg ggg ggt			543
Leu Asp Phe Pro Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly			
145	150	155	
tat atg ggt tta ggt ttg ggg gtt gta gcg cat ggg gtg aat tac acg			591
Tyr Met Gly Leu Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr			
160	165	170	
gcg gaa tgg ggg atg tct ttt aac gca gga ttg gct cta acg gta tta			639
Ala Glu Trp Gly Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu			
175	180	185	
gaa aaa aac cgc att gaa ttt gga ttt aaa att ttg aat aat ttc cct			687
Glu Lys Asn Arg Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro			
190	195	200	
ttt ttg caa tct aat tct tca aaa gag act tgg tgg gga gct atg gca			735
Phe Leu Gln Ser Asn Ser Ser Lys Glu Thr Trp Trp Gly Ala Met Ala			
205	210	215	220
aac att ggg tat caa tat gtg ttc taaaaaata agaaatctca ttttatgctt			789
Asn Ile Gly Tyr Gln Tyr Val Phe			
225			
tggttttatg ttgggcttgc acgctgaaga aaatacgact gaaggaaata tgactgaaga			849
aaatatctct aaagacgctc			869
<210> 126			
<211> 228			
<212> PRT			
<213> Helicobacter pylori			
<400> 126			
Met Gly Phe Tyr Ala Gly Leu Asn Ala Leu Asp Tyr Asp Thr Ile Asp			
1 5 10 15			
Pro Lys Tyr Tyr Lys Tyr Ile Lys Tyr Tyr Lys Ala Tyr Glu Asp Lys			
20 25 30			
Glu Val Glu Glu Leu Ile Arg Asp Leu Lys Arg Ala Asn Ala Lys Ser			
35 40 45			
Gly Leu Ile Leu Gly Ile Asn Thr Gly Phe Phe Tyr Asn His Glu Ile			
50 55 60			
Met Val Arg Thr Asn Ser Ser Ile Thr Gly Asn Ile Leu Asn Tyr			
65 70 75 80			
Leu Phe Ala Tyr Gly Leu Arg Phe Gly Tyr Gln Thr Phe Arg Pro Ser			
85 90 95			

Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly Arg Arg Ile Tyr
 100 105 110
 Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly Phe Gly Asp Val
 115 120 125
 Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu Leu Asp Phe Pro
 130 135 140
 Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly Tyr Met Gly Leu
 145 150 155 160
 Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr Ala Glu Trp Gly
 165 170 175
 Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu Glu Lys Asn Arg
 180 185 190
 Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro Phe Leu Gln Ser
 195 200 205
 Asn Ser Ser Lys Glu Thr Trp Trp Gly Ala Met Ala Asn Ile Gly Tyr
 210 215 220
 Gln Tyr Val Phe
 225

<210> 127
 <211> 1171
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (89)...(1096)

<400> 127
 ggaaagaatt gattcaaaac gctatcaaac aatacgctga tgatgtgaaa aagggaaact 60
 tccctaacga attagaaagt tatcatta atg aaa gaa cgg ata gtc aat tta 112
 Met Lys Glu Arg Ile Val Asn Leu
 1 5
 gaa act ttg gat ttt gaa att tct caa gaa gtg agt ttg cgc cct agt 160
 Glu Thr Leu Asp Phe Glu Ile Ser Gln Glu Val Ser Leu Arg Pro Ser
 10 15 20
 ctt tgg gaa gat ttt atc ggt caa gaa aag att aaa agc aat ttg caa 208
 Leu Trp Glu Asp Phe Ile Gly Gln Glu Lys Ile Lys Ser Asn Leu Gln
 25 30 35 40
 att tct att tgc gcg gct aaa aaa cgc caa gaa agt ttg gat cac atg 256
 Ile Ser Ile Cys Ala Ala Lys Lys Arg Gln Glu Ser Leu Asp His Met
 45 50 55
 ctt ttt ttt ggc ccg ccc ggt ttg ggt aaa act tca atc agc cat atc 304
 Leu Phe Phe Gly Pro Pro Gly Leu Gly Lys Thr Ser Ile Ser His Ile
 60 65 70
 atc gct aaa gaa atg gaa acc aat atc aag atc acc gcc gct ccc atg 352
 Ile Ala Lys Glu Met Glu Thr Asn Ile Lys Ile Thr Ala Ala Pro Met
 75 80 85
 ata gaa aaa agc ggt gat tta gcc gcc att ttg acc aat ttg caa gct 400
 Ile Glu Lys Ser Gly Asp Leu Ala Ala Ile Leu Thr Asn Leu Gln Ala
 90 95 100
 aaa gac att ctt ttt att gat gaa atc cac cgg ctc agc cca gcg att 448

Lys	Asp	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Arg	Leu	Ser	Pro	Ala	Ile		
105					110					115					120		
gaa	gag	gtt	tta	tac	ccg	gcg	atg	gaa	gat	ttt	agg	ttg	gat	att	atc		496
Glu	Glu	Val	Leu	Tyr	Pro	Ala	Met	Glu	Asp	Phe	Arg	Leu	Asp	Ile	Ile		
				125					130					135			
ata	ggc	tca	ggc	cca	gcg	gct	caa	acc	att	aaa	att	gat	tta	ccc	cct		544
Ile	Gly	Ser	Gly	Pro	Ala	Ala	Gln	Thr	Ile	Lys	Ile	Asp	Leu	Pro	Pro		
			140					145					150				
ttc	act	ctc	atc	ggc	gct	acc	acc	aga	gcc	gga	atg	ctc	tct	aac	ccc		592
Phe	Thr		Leu	Ile	Gly	Ala	Thr	Arg	Ala	Gly	Met	Leu	Ser	Asn	Pro		
			155					160					165				
tta	aga	gac	aga	ttt	ggc	atg	agt	ttt	aga	atg	caa	ttt	tat	aac	cct		640
Leu	Arg	Asp	Arg	Phe	Gly	Met	Ser	Phe	Arg	Met	Gln	Phe	Tyr	Asn	Pro		
	170					175					180						
agc	gaa	ctg	gcc	ctc	atc	att	aaa	aaa	gct	gcc	gtt	aaa	ctc	aac	caa		688
Ser	Glu	Leu	Ala	Leu	Ile	Ile	Lys	Lys	Ala	Ala	Val	Lys	Leu	Asn	Gln		
185					190					195				200			
gac	atc	aaa	caa	gaa	agt	gct	gat	gaa	atc	gct	aaa	agg	agt	aga	ggc		736
Asp	Ile	Lys	Gln	Glu	Ser	Ala	Asp	Glu	Ile	Ala	Lys	Arg	Ser	Arg	Gly		
			205					210						215			
acg	cca	agg	atc	gct	tta	agg	ctt	tta	aaa	agg	gtg	cgc	gat	ttt	gcg		784
Thr	Pro	Arg	Ile	Ala	Leu	Arg	Leu	Leu	Lys	Arg	Val	Arg	Asp	Phe	Ala		
			220				225						230				
cta	gtc	aaa	aat	tca	agc	ttg	atg	gat	tta	aac	atc	act	ttg	cat	gct		832
Leu	Val	Lys	Asn	Ser	Ser	Leu	Met	Asp	Leu	Asn	Ile	Thr	Leu	His	Ala		
		235					240					245					
ttg	aat	gaa	tta	ggc	gtg	aat	gaa	tta	ggc	ttt	gat	gaa	gcg	gat	ttg		880
Leu	Asn	Glu	Leu	Gly	Val	Asn	Glu	Leu	Gly	Phe	Asp	Glu	Ala	Asp	Leu		
	250					255					260						
gcg	tat	tta	tct	ttg	ttg	gct	aac	gct	caa	gga	aag	ccg	gtg	ggt	ttg		928
Ala	Tyr	Leu	Ser	Leu	Leu	Ala	Asn	Ala	Gln	Gly	Lys	Pro	Val	Gly	Leu		
265				270					275					280			
aac	acg	att	gca	gca	tct	atg	aga	gaa	gat	gaa	ggc	acg	att	gaa	gac		976
Asn	Thr	Ile	Ala	Ala	Ser	Met	Arg	Glu	Asp	Glu	Gly	Thr	Ile	Glu	Asp		
			285					290						295			
gtg	att	gag	cct	ttt	tta	ctc	gct	aat	ggt	tat	tta	gag	cgc	acc	gct		1024
Val	Ile	Glu	Pro	Phe	Leu	Leu	Ala	Asn	Gly	Tyr	Leu	Glu	Arg	Thr	Ala		
			300					305					310				
aaa	ggc	aga	atc	gcc	acg	cct	aaa	acc	cat	gag	ctc	tta	aaa	atc	ccc		1072
Lys	Gly	Arg	Ile	Ala	Thr	Pro	Lys	Thr	His	Glu	Leu	Leu	Lys	Ile	Pro		
		315				320						325					
act	tta	aac	ccc	caa	act	tta	ttt	taat	ctt	ggt	tagaa	agaaa	attac	actac			1126
Thr	Leu	Asn	Pro	Gln	Thr	Leu	Phe										
	330					335											

aataacgata aaatttttaaa ggggtgtaaaa gtagattgtt atgtt

1171

<210> 128
 <211> 336
 <212> PRT
 <213> Helicobacter pylori

<400> 128
 Met Lys Glu Arg Ile Val Asn Leu Glu Thr Leu Asp Phe Glu Ile Ser
 1 5 10 15
 Gln Glu Val Ser Leu Arg Pro Ser Leu Trp Glu Asp Phe Ile Gly Gln
 20 25 30
 Glu Lys Ile Lys Ser Asn Leu Gln Ile Ser Ile Cys Ala Ala Lys Lys
 35 40 45
 Arg Gln Glu Ser Leu Asp His Met Leu Phe Phe Gly Pro Pro Gly Leu
 50 55 60
 Gly Lys Thr Ser Ile Ser His Ile Ile Ala Lys Glu Met Glu Thr Asn
 65 70 75 80
 Ile Lys Ile Thr Ala Ala Pro Met Ile Glu Lys Ser Gly Asp Leu Ala
 85 90 95
 Ala Ile Leu Thr Asn Leu Gln Ala Lys Asp Ile Leu Phe Ile Asp Glu
 100 105 110
 Ile His Arg Leu Ser Pro Ala Ile Glu Glu Val Leu Tyr Pro Ala Met
 115 120 125
 Glu Asp Phe Arg Leu Asp Ile Ile Ile Gly Ser Gly Pro Ala Ala Gln
 130 135 140
 Thr Ile Lys Ile Asp Leu Pro Pro Phe Thr Leu Ile Gly Ala Thr Thr
 145 150 155 160
 Arg Ala Gly Met Leu Ser Asn Pro Leu Arg Asp Arg Phe Gly Met Ser
 165 170 175
 Phe Arg Met Gln Phe Tyr Asn Pro Ser Glu Leu Ala Leu Ile Ile Lys
 180 185 190
 Lys Ala Ala Val Lys Leu Asn Gln Asp Ile Lys Gln Glu Ser Ala Asp
 195 200 205
 Glu Ile Ala Lys Arg Ser Arg Gly Thr Pro Arg Ile Ala Leu Arg Leu
 210 215 220
 Leu Lys Arg Val Arg Asp Phe Ala Leu Val Lys Asn Ser Ser Leu Met
 225 230 235 240
 Asp Leu Asn Ile Thr Leu His Ala Leu Asn Glu Leu Gly Val Asn Glu
 245 250 255
 Leu Gly Phe Asp Glu Ala Asp Leu Ala Tyr Leu Ser Leu Leu Ala Asn
 260 265 270
 Ala Gln Gly Lys Pro Val Gly Leu Asn Thr Ile Ala Ala Ser Met Arg
 275 280 285
 Glu Asp Glu Gly Thr Ile Glu Asp Val Ile Glu Pro Phe Leu Leu Ala
 290 295 300
 Asn Gly Tyr Leu Glu Arg Thr Ala Lys Gly Arg Ile Ala Thr Pro Lys
 305 310 315 320
 Thr His Glu Leu Leu Lys Ile Pro Thr Leu Asn Pro Gln Thr Leu Phe
 325 330 335

<210> 129
 <211> 989
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (111)...(869)

<400> 129
agttttccaat gaagaagcct taaacaaaga agttttcaagc gatgaatccc ctaaagaagt 60
ccaattagca accgataaca acaccaaaga acacgacaaa gaaaaagaga atg ttt 116
Met Phe
1

gaa gat tta aaa ccg cat tta cag gaa tta aga aag cgt ttg atg gtt 164
Glu Asp Leu Lys Pro His Leu Gln Glu Leu Arg Lys Arg Leu Met Val
5 10 15

tct gta gga acg att cta gtg gcg ttt ttg ggg tgc ttt cat ttt tgg 212
Ser Val Gly Thr Ile Leu Val Ala Phe Leu Gly Cys Phe His Phe Trp
20 25 30

aaa agt att ttt gaa ttt gtt aaa aat tcc tat aaa ggc acg ctc att 260
Lys Ser Ile Phe Glu Phe Val Lys Asn Ser Tyr Lys Gly Thr Leu Ile
35 40 45 50

cag ctc tcc cct att gaa ggg gtc atg gta gcg gtt aaa atc agt ttt 308
Gln Leu Ser Pro Ile Glu Gly Val Met Val Ala Val Lys Ile Ser Phe
55 60 65

tca gcc gct atc gtc att tcc atg ccc att att ttt tgg caa tta tgg 356
Ser Ala Ala Ile Val Ile Ser Met Pro Ile Ile Phe Trp Gln Leu Trp
70 75 80

ctc ttt atc gct cca ggg ctt tac aag aat gaa aaa aaa gtg att ttg 404
Leu Phe Ile Ala Pro Gly Leu Tyr Lys Asn Glu Lys Lys Val Ile Leu
85 90 95

cct ttt gtg ttt ttt ggg agt ggg atg ttt ttg att ggg gcg gcg ttt 452
Pro Phe Val Phe Phe Gly Ser Gly Met Phe Leu Ile Gly Ala Ala Phe
100 105 110

tct tat tat gtg gtg ttc cct ttc att att gaa tac tta gcc act ttt 500
Ser Tyr Tyr Val Val Phe Pro Phe Ile Ile Glu Tyr Leu Ala Thr Phe
115 120 125 130

ggg agc gat gtg ttt gcg gct aat att tct gcg tcc agt tac gtg agc 548
Gly Ser Asp Val Phe Ala Ala Asn Ile Ser Ala Ser Ser Tyr Val Ser
135 140 145

ttt ttc acg cgc ttg att tta ggc ttt ggc gtg gcg ttt gaa ttg cct 596
Phe Phe Thr Arg Leu Ile Leu Gly Phe Gly Val Ala Phe Glu Leu Pro
150 155 160

gtt ttg gcg tat ttt ttg gct aaa gtg ggc ttg att act gat gcg agc 644
Val Leu Ala Tyr Phe Leu Ala Lys Val Gly Leu Ile Thr Asp Ala Ser
165 170 175

ttg aaa gcg tat ttt aaa tac gct att gta gtg att ttt att gta gca 692
Leu Lys Ala Tyr Phe Lys Tyr Ala Ile Val Val Ile Phe Ile Val Ala
180 185 190

gcc att atc act ccc cct gat gtg gtg agt caa atc ttt atg gcg ttg 740
Ala Ile Ile Thr Pro Asp Val Val Ser Gln Ile Phe Met Ala Leu
195 200 205 210

ccc tta gtg ggg ctt tat ggg ctt tct att tta atc gcc aaa atg gtc 788

Pro Leu Val Gly Leu Tyr Gly Leu Ser Ile Leu Ile Ala Lys Met Val
215 220 225

aat ccg gct ccc aaa gat aac gaa aat aac aac gaa aat aat aac gaa 836
Asn Pro Ala Pro Lys Asp Asn Glu Asn Asn Glu Asn Asn Asn Glu
230 235 240

aat aac acc aaa gag aat aca aag agc gag tcg tagttgaaag aatttgattt 889
Asn Asn Thr Lys Glu Asn Thr Lys Ser Glu Ser
245 250

agaaaagctat gattattatt tgcctaagga attgatcgca agctaccccg ttttgcccaa 949
agaaaaggct aaattactcg tctatgaaag gcgttcgcaa 989

<210> 130
<211> 253
<212> PRT
<213> Helicobacter pylori

<400> 130

Met Phe Glu Asp Leu Lys Pro His Leu Gln Glu Leu Arg Lys Arg Leu
1 5 10 15
Met Val Ser Val Gly Thr Ile Leu Val Ala Phe Leu Gly Cys Phe His
20 25 30
Phe Trp Lys Ser Ile Phe Glu Phe Val Lys Asn Ser Tyr Lys Gly Thr
35 40 45
Leu Ile Gln Leu Ser Pro Ile Glu Gly Val Met Val Ala Val Lys Ile
50 55 60
Ser Phe Ser Ala Ala Ile Val Ile Ser Met Pro Ile Ile Phe Trp Gln
65 70 75 80
Leu Trp Leu Phe Ile Ala Pro Gly Leu Tyr Lys Asn Glu Lys Lys Val
85 90 95
Ile Leu Pro Phe Val Phe Phe Gly Ser Gly Met Phe Leu Ile Gly Ala
100 105 110
Ala Phe Ser Tyr Tyr Val Val Phe Pro Phe Ile Ile Glu Tyr Leu Ala
115 120 125
Thr Phe Gly Ser Asp Val Phe Ala Ala Asn Ile Ser Ala Ser Ser Tyr
130 135 140
Val Ser Phe Phe Thr Arg Leu Ile Leu Gly Phe Gly Val Ala Phe Glu
145 150 155 160
Leu Pro Val Leu Ala Tyr Phe Leu Ala Lys Val Gly Leu Ile Thr Asp
165 170 175
Ala Ser Leu Lys Ala Tyr Phe Lys Tyr Ala Ile Val Val Ile Phe Ile
180 185 190
Val Ala Ala Ile Ile Thr Pro Pro Asp Val Val Ser Gln Ile Phe Met
195 200 205
Ala Leu Pro Leu Val Gly Leu Tyr Gly Leu Ser Ile Leu Ile Ala Lys
210 215 220
Met Val Asn Pro Ala Pro Lys Asp Asn Glu Asn Asn Asn Glu Asn Asn
225 230 235 240
Asn Glu Asn Asn Thr Lys Glu Asn Thr Lys Ser Glu Ser
245 250

<210> 131
<211> 655
<212> DNA
<213> Helicobacter pylori

<220>

<221> CDS
 <222> (31)...(600)

<400> 131

gtgcattatt taagaatttt aatactgagt atg agt ttt tta aat att tta aat	54
Met Ser Phe Leu Asn Ile Leu Asn	
1 5	
gct gaa aat ttg agt tat atg tct tct tct tat caa ata ggc acg gtg	102
Ala Glu Asn Leu Ser Tyr Met Ser Ser Ser Tyr Gln Ile Gly Thr Val	
10 15 20	
ttt atg cgc cct tta aac acc aac aag ctt tta caa ggg gct tca atc	150
Phe Met Arg Pro Leu Asn Thr Asn Lys Leu Leu Gln Gly Ala Ser Ile	
25 30 35 40	
ctt caa ggc tat gaa gtg aat cct aaa aac gat tgg gct tat tct agg	198
Leu Gln Gly Tyr Glu Val Asn Pro Lys Asn Asp Trp Ala Tyr Ser Arg	
45 50 55	
tat tat ttc ttt ata gat tat ggc aat gtg ctt ttt aat aat gac tct	246
Tyr Tyr Phe Phe Ile Asp Tyr Gly Asn Val Leu Phe Asn Asn Asp Ser	
60 65 70	
act tta caa gcg aac atg ttc act tat ggg gtg gga ggg gat ttt atg	294
Thr Leu Gln Ala Asn Met Phe Thr Tyr Gly Val Gly Gly Asp Phe Met	
75 80 85	
gtc gcc tac gct aaa aac cct atc aac cgc tgg gct ttt ttc ttt ggc	342
Val Ala Tyr Ala Lys Asn Pro Ile Asn Arg Trp Ala Phe Phe Phe Gly	
90 95 100	
ttg caa ctg gcc gct aac aca tgg ata ctc aac aat aaa gtc aaa gat	390
Leu Gln Leu Ala Ala Asn Thr Trp Ile Leu Asn Asn Lys Val Lys Asp	
105 110 115 120	
ttg gtg gtg aat act tgg gat tca tta aaa gat ttc aat ttt cac aac	438
Leu Val Val Asn Thr Trp Asp Ser Leu Lys Asp Phe Asn Phe His Asn	
125 130 135	
act tat ttc agg gct att ggg aag ttt ggg gtg cag ttt cgc acg atc	486
Thr Tyr Phe Arg Ala Ile Gly Lys Phe Gly Val Gln Phe Arg Thr Ile	
140 145 150	
gtt ttg tat cat aag gtg gat gta gaa att ggc atg aaa atc ttt cta	534
Val Leu Tyr His Lys Val Asp Val Glu Ile Gly Met Lys Ile Phe Leu	
155 160 165	
act cct gaa agg cgc agt ttg ttt gaa agg agc ttt ttg ttt ttt gtt	582
Thr Pro Glu Arg Arg Ser Leu Phe Glu Arg Ser Phe Leu Phe Phe Val	
170 175 180	
tcg cat tcg tgg cat ttt taaatggcgg agagagaggg attcgaaccc	630
Ser His Ser Trp His Phe	
185 190	
tcgaaggctt gcaccttaca cgcgt	655

<210> 132

<211> 190
 <212> PRT
 <213> Helicobacter pylori

<400> 132
 Met Ser Phe Leu Asn Ile Leu Asn Ala Glu Asn Leu Ser Tyr Met Ser
 1 5 10 15
 Ser Ser Tyr Gln Ile Gly Thr Val Phe Met Arg Pro Leu Asn Thr Asn
 20 25 30
 Lys Leu Leu Gln Gly Ala Ser Ile Leu Gln Gly Tyr Glu Val Asn Pro
 35 40 45
 Lys Asn Asp Trp Ala Tyr Ser Arg Tyr Tyr Phe Phe Ile Asp Tyr Gly
 50 55 60
 Asn Val Leu Phe Asn Asn Asp Ser Thr Leu Gln Ala Asn Met Phe Thr
 65 70 75 80
 Tyr Gly Val Gly Gly Asp Phe Met Val Ala Tyr Ala Lys Asn Pro Ile
 85 90 95
 Asn Arg Trp Ala Phe Phe Phe Gly Leu Gln Leu Ala Ala Asn Thr Trp
 100 105 110
 Ile Leu Asn Asn Lys Val Lys Asp Leu Val Val Asn Thr Trp Asp Ser
 115 120 125
 Leu Lys Asp Phe Asn Phe His Asn Thr Tyr Phe Arg Ala Ile Gly Lys
 130 135 140
 Phe Gly Val Gln Phe Arg Thr Ile Val Leu Tyr His Lys Val Asp Val
 145 150 155 160
 Glu Ile Gly Met Lys Ile Phe Leu Thr Pro Glu Arg Arg Ser Leu Phe
 165 170 175
 Glu Arg Ser Phe Leu Phe Phe Val Ser His Ser Trp His Phe
 180 185 190

<210> 133
 <211> 830
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (31)...(714)

<400> 133
 aaagcactat attaagatta ggatcattta atg gca gat aaa gaa ata ctg att 54
 Met Ala Asp Lys Glu Ile Leu Ile
 1 5
 ttt gta gaa ggt cca agc gat aag gtg ttt tta gaa gtt tat ctg tat 102
 Phe Val Glu Gly Pro Ser Asp Lys Val Phe Leu Glu Val Tyr Leu Tyr
 10 15 20
 ttt cta gaa aga ttt cca atc aaa aac ttt aaa gtg caa aat gta gat 150
 Phe Leu Glu Arg Phe Pro Ile Lys Asn Phe Lys Val Gln Asn Val Asp
 25 30 35 40
 gga aaa gat aac ctg tct aaa cga ttg ctt gaa att gaa aaa tac gat 198
 Gly Lys Asp Asn Leu Ser Lys Arg Leu Leu Glu Ile Glu Lys Tyr Asp
 45 50 55
 aaa aca ctt atc att ttt gat gcg gat aaa gac tat gag agt aat aaa 246
 Lys Thr Leu Ile Ile Phe Asp Ala Asp Lys Asp Tyr Glu Ser Asn Lys
 60 65 70

65					70					75				80
Glu	Ser	Lys	Gln	Thr	Ile	Ser	Glu	Glu	Gln	Ile	Phe	Leu	Phe	Pro Asn
				85					90					95
Asn	Gln	Asp	Asp	Gly	Asp	Leu	Glu	Thr	Leu	Leu	Leu	Lys	Ile	Ala Asn
			100						105				110	
His	Lys	Glu	Phe	Ile	Asn	Cys	Phe	Glu	Ser	Tyr	Leu	Asp	Cys	Ile Lys
		115					120					125		
Lys	Lys	Glu	His	Tyr	Lys	Pro	Ile	Lys	Asn	Ile	Arg	Lys	Ser	Lys Trp
		130				135					140			
Tyr	Ala	Tyr	Leu	Glu	Ala	Leu	Gly	Leu	Glu	Lys	Phe	Phe	Gln	Tyr Thr
145					150					155				160
Trp	Asp	Thr	Lys	Lys	Lys	Asn	Asn	Lys	Lys	Lys	Leu	Ile	Ile	Asp Asp
				165					170					175
Lys	Asp	Gly	Asp	Glu	Ile	Glu	Ile	Lys	Asp	Gln	Tyr	Lys	Gly	Asp Tyr
			180					185					190	
Glu	Glu	Leu	Lys	Lys	Val	Leu	Asp	Leu	Asn	Ser	Lys	Ser	Leu	Ile Pro
		195				200					205			
Leu	Lys	Asn	Phe	Leu	Gly	Gln	Phe	Ala	Glu	Asn	Asn	Gln	Lys	Thr Asn
		210				215					220			
Pro	Lys	Ile	Phe											
225														

<210> 135
 <211> 1349
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (78)...(1298)

<400> 135	
aagaacaaat tgagcctgct accgctctca ctcaatggcc gcaaaaaacaa gaaaagaaaa	60
aatcataagg aaaaaat atg gca aaa agt att gaa ttg caa gag ata gaa	110
Met Ala Lys Ser Ile Glu Leu Gln Glu Ile Glu	
1 5 10	
gtg tgg gat ggc aat acc gct agt tct aac gct tta aga cag gct caa	158
Val Trp Asp Gly Asn Thr Ala Ser Ser Asn Ala Leu Arg Gln Ala Gln	
15 20 25	
att gat gtc atc gca gcc tat cct atc acc cca tca acg ccc att gtg	206
Ile Asp Val Ile Ala Ala Tyr Pro Ile Thr Pro Ser Thr Pro Ile Val	
30 35 40	
caa aat tat ggc tcg ttt aag gat aat ggc tat gtt gat ggc gaa ttc	254
Gln Asn Tyr Gly Ser Phe Lys Asp Asn Gly Tyr Val Asp Gly Glu Phe	
45 50 55	
gtt tta gtg gaa tct gag cat gcc gcc atg agc gca tgc gtg gga gct	302
Val Leu Val Glu Ser Glu His Ala Ala Met Ser Ala Cys Val Gly Ala	
60 65 70 75	
gcc gca gct gga ggg aga gtc agc act gcg act agc tct caa ggt ttg	350
Ala Ala Ala Gly Gly Arg Val Ser Thr Ala Thr Ser Ser Gln Gly Leu	
80 85 90	
gcg tta atg gta gag gtt tta tac cag gct tct gga atg cgt ttg cct	398
Ala Leu Met Val Glu Val Leu Tyr Gln Ala Ser Gly Met Arg Leu Pro	

95						100						105						
atc Ile	gtt Val	ttg Leu	aat Asn	tta Leu	gtc Val	aat Asn	cgt Arg	gct Ala	tta Leu	gca Ala	gcc Ala	cct Pro	ttg Leu	aat Asn	atc Ile	446		
110						115						120						
cat His	ggc Gly	gat Asp	cat His	tct Ser	gat Asp	atg Met	tat Tyr	tta Leu	agc Ser	agg Arg	gat Asp	tct Ser	ggg Gly	tgg Trp	ata Ile	494		
125						130						135						
agt Ser	tta Leu	tgc Cys	aca Thr	tgc Cys	aac Asn	ccc Pro	caa Gln	gaa Glu	gct Ala	tat Tyr	gat Asp	ttc Phe	act Thr	tta Leu	atg Met	542		
140						145						150						
gcg Ala	ttt Phe	aga Arg	atc Ile	gca Ala	gag Glu	cat His	caa Gln	aag Lys	gtg Val	cgc Arg	gtg Val	cct Pro	act Thr	att Ile	gtc Val	590		
160						165						170						
aat Asn	caa Gln	gac Asp	ggg Gly	ttt Phe	tta Leu	tgc Cys	tcg Ser	cac His	acc Thr	gtg Val	caa Gln	aat Asn	gtc Val	cgc Arg	cct Pro	638		
175						180						185						
ttg Leu	agc Ser	gat Asp	gca Ala	gtg Val	gct Ala	tac Tyr	caa Gln	ttc Phe	gtg Val	ggc Gly	gaa Glu	tac Tyr	caa Gln	acc Thr	aag Lys	686		
190						195						200						
cat His	tcc Ser	ctt Leu	ttg Leu	gat Asp	ttt Phe	gat Asp	aaa Lys	ccg Pro	gta Val	agc Ser	tat Tyr	ggc Gly	gcg Ala	caa Gln	gct Ala	734		
205						210						215						
gaa Glu	gaa Glu	gaa Glu	tgg Trp	cat His	tat Tyr	gag Glu	cat His	aaa Lys	gcc Ala	caa Gln	ctc Leu	cac His	cat His	gcc Ala	atc Ile	782		
220						225						230						
atg Met	agc Ser	gcg Ala	tct Ser	tct Ser	gtg Val	att Ile	gaa Glu	gaa Glu	gtg Val	ttc Phe	aat Asn	gat Asp	ttc Phe	gct Ala	aaa Lys	830		
240						245						250						
ctc Leu	aca Thr	ggc Gly	agg Arg	caa Gln	tac Tyr	cat His	tta Leu	acc Thr	aaa Lys	act Thr	ttc Phe	cag Gln	cta Leu	gaa Glu	gac Asp	878		
255						260						265						
gct Ala	gaa Glu	atc Ile	gct Ala	atc Ile	ttt Phe	gcg Ala	tta Leu	ggc Gly	act Thr	act Thr	tat Tyr	gaa Glu	tca Ser	gcg Ala	atc Ile	926		
270						275						280						
gta Val	gcg Ala	gct Ala	aaa Lys	gaa Glu	atg Met	cgt Arg	aaa Lys	aaa Lys	ggc Gly	att Ile	aag Lys	gcc Ala	ggc Gly	gtg Val	gct Ala	974		
285						290						295						
acc Thr	atc Ile	cat His	tcc Ser	ttg Leu	cgc Arg	ccc Pro	ttc Phe	cct Pro	tat Tyr	gaa Glu	aga Arg	tta Leu	ggg Gly	cag Gln	gat Asp	1022		
300						305						310						
ttg Leu	aaa Lys	aat Asn	ctt Leu	aaa Lys	gct Ala	tta Leu	gcg Ala	att Ile	tta Leu	gac Asp	aag Lys	agc Ser	tct Ser	cca Pro	gcg Ala	1070		
320						325						330						
ggc	act	atg	ggg	gcg	atg	ttt	aat	gaa	gta	acg	agc	gcg	gtg	tat	caa	1118		

Gly Thr Met Gly Ala Met Phe Asn Glu Val Thr Ser Ala Val Tyr Gln	
335 340 345	
acg caa ggg act aaa cac ccc gtg gtg tct aac tac att tat ggt tta	1166
Thr Gln Gly Thr Lys His Pro Val Val Ser Asn Tyr Ile Tyr Gly Leu	
350 355 360	
ggc gaa agg gat atg acg atc gcg cat tta tgc gaa att ttt gaa gaa	1214
Gly Glu Arg Asp Met Thr Ile Ala His Leu Cys Glu Ile Phe Glu Glu	
365 370 375	
atc aat gaa gac gct ctt aaa ggc acg ctc acg cac cct acc caa caa	1262
Ile Asn Glu Asp Ala Leu Lys Gly Thr Leu Thr His Pro Thr Gln Gln	
380 385 390 395	
ttc gta ggc ttg cac ggc cct aaa atg agc ttt ttt taaaaaggaa	1308
Phe Val Gly Leu His Gly Pro Lys Met Ser Phe Phe	
400 405	
atatcatgggt aaaagaagtc aaaacactca aagggttttag c	1349

<210> 136
 <211> 407
 <212> PRT
 <213> Helicobacter pylori

Met Ala Lys Ser Ile Glu Leu Gln Glu Ile Glu Val Trp Asp Gly Asn	
1 5 10 15	
Thr Ala Ser Ser Asn Ala Leu Arg Gln Ala Gln Ile Asp Val Ile Ala	
20 25 30	
Ala Tyr Pro Ile Thr Pro Ser Thr Pro Ile Val Gln Asn Tyr Gly Ser	
35 40 45	
Phe Lys Asp Asn Gly Tyr Val Asp Gly Glu Phe Val Leu Val Glu Ser	
50 55 60	
Glu His Ala Ala Met Ser Ala Cys Val Gly Ala Ala Ala Gly Gly	
65 70 75 80	
Arg Val Ser Thr Ala Thr Ser Ser Gln Gly Leu Ala Leu Met Val Glu	
85 90 95	
Val Leu Tyr Gln Ala Ser Gly Met Arg Leu Pro Ile Val Leu Asn Leu	
100 105 110	
Val Asn Arg Ala Leu Ala Ala Pro Leu Asn Ile His Gly Asp His Ser	
115 120 125	
Asp Met Tyr Leu Ser Arg Asp Ser Gly Trp Ile Ser Leu Cys Thr Cys	
130 135 140	
Asn Pro Gln Glu Ala Tyr Asp Phe Thr Leu Met Ala Phe Arg Ile Ala	
145 150 155 160	
Glu His Gln Lys Val Arg Val Pro Thr Ile Val Asn Gln Asp Gly Phe	
165 170 175	
Leu Cys Ser His Thr Val Gln Asn Val Arg Pro Leu Ser Asp Ala Val	
180 185 190	
Ala Tyr Gln Phe Val Gly Glu Tyr Gln Thr Lys His Ser Leu Leu Asp	
195 200 205	
Phe Asp Lys Pro Val Ser Tyr Gly Ala Gln Ala Glu Glu Glu Trp His	
210 215 220	
Tyr Glu His Lys Ala Gln Leu His His Ala Ile Met Ser Ala Ser Ser	
225 230 235 240	
Val Ile Glu Glu Val Phe Asn Asp Phe Ala Lys Leu Thr Gly Arg Gln	
245 250 255	

Tyr His Leu Thr Lys Thr Phe Gln Leu Glu Asp Ala Glu Ile Ala Ile
 260 265 270
 Phe Ala Leu Gly Thr Thr Tyr Glu Ser Ala Ile Val Ala Ala Lys Glu
 275 280 285
 Met Arg Lys Lys Gly Ile Lys Ala Gly Val Ala Thr Ile His Ser Leu
 290 295 300
 Arg Pro Phe Pro Tyr Glu Arg Leu Gly Gln Asp Leu Lys Asn Leu Lys
 305 310 315 320
 Ala Leu Ala Ile Leu Asp Lys Ser Ser Pro Ala Gly Thr Met Gly Ala
 325 330 335
 Met Phe Asn Glu Val Thr Ser Ala Val Tyr Gln Thr Gln Gly Thr Lys
 340 345 350
 His Pro Val Val Ser Asn Tyr Ile Tyr Gly Leu Gly Glu Arg Asp Met
 355 360 365
 Thr Ile Ala His Leu Cys Glu Ile Phe Glu Glu Ile Asn Glu Asp Ala
 370 375 380
 Leu Lys Gly Thr Leu Thr His Pro Thr Gln Gln Phe Val Gly Leu His
 385 390 395 400
 Gly Pro Lys Met Ser Phe Phe
 405

<210> 137
 <211> 948
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)...(855)

<400> 137
 aaa att gaa gtt tta agg ggt ttt ttg aaa cga gcg tta tac tta att 48
 Lys Ile Glu Val Leu Arg Gly Phe Leu Lys Arg Ala Leu Tyr Leu Ile
 1 5 10 15
 tta ggg ctt ttt tac acg ctt aat gca gag agc ttt aaa gat gtt ttg 96
 Leu Gly Leu Phe Tyr Thr Leu Asn Ala Glu Ser Phe Lys Asp Val Leu
 20 25 30
 act aaa gtg gat tac act ttt ttt aat aaa aag gtg gtt tcg ccc atc 144
 Thr Lys Val Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile
 35 40 45
 aaa cgc tat gcg gat aga tcg gcg ttt tat ctg ggg ctt ggg tat caa 192
 Lys Arg Tyr Ala Asp Arg Ser Ala Phe Tyr Leu Gly Leu Gly Tyr Gln
 50 55 60
 tta ggg agc att cag cac aac tct agc aac ttg aat tta tcc cag caa 240
 Leu Gly Ser Ile Gln His Asn Ser Ser Asn Leu Asn Leu Ser Gln Gln
 65 70 75 80
 ttc aat aag agt cag att att ttc agc gat agt cta agc cct gtt ttt 288
 Phe Asn Lys Ser Gln Ile Ile Phe Ser Asp Ser Leu Ser Pro Val Phe
 85 90 95
 aaa aat tcg tat gtg tct aat ggc ctt ggc gtg caa gtg ggc tat aag 336
 Lys Asn Ser Tyr Val Ser Asn Gly Leu Gly Val Gln Val Gly Tyr Lys
 100 105 110

tgg gtg ggt aag cat gaa gag acg aaa tgg ttt ggc ttc agg tgg ggg	384
Trp Val Gly Lys His Glu Glu Thr Lys Trp Phe Gly Phe Arg Trp Gly	
115 120 125	
ctg ttt tat gat ttg agc gcc tct ctt tat ggc caa aaa gaa tca cag	432
Leu Phe Tyr Asp Leu Ser Ala Ser Leu Tyr Gly Gln Lys Glu Ser Gln	
130 135 140	
tct gtc atc att tcc act tac ggc act tat atg gat tta tta ttg aac	480
Ser Val Ile Ile Ser Thr Tyr Gly Thr Tyr Met Asp Leu Leu Leu Asn	
145 150 155 160	
gct tat aat ggg gat aag ttt ttt gct ggg ttc aat ctg ggg att gct	528
Ala Tyr Asn Gly Asp Lys Phe Phe Ala Gly Phe Asn Leu Gly Ile Ala	
165 170 175	
ttt gct gga gtg tat gac aaa gtg agc gat gcg tta ttg tat caa gcc	576
Phe Ala Gly Val Tyr Asp Lys Val Ser Asp Ala Leu Leu Tyr Gln Ala	
180 185 190	
ctt ctt tta gac act ttt ggc ggg aaa gtg gat cca aat ggc ttc cag	624
Leu Leu Leu Asp Thr Phe Gly Gly Lys Val Asp Pro Asn Gly Phe Gln	
195 200 205	
ttt ttg gta aat tta ggg gtt cgt tta ggg aat aag cac aac caa ttt	672
Phe Leu Val Asn Leu Gly Val Arg Leu Gly Asn Lys His Asn Gln Phe	
210 215 220	
ggc ttt ggg att aaa atc cct act tat tat ttt aac cat tat tat tcc	720
Gly Phe Gly Ile Lys Ile Pro Thr Tyr Tyr Phe Asn His Tyr Tyr Ser	
225 230 235 240	
atg aat aac att agc aat aat agt gaa gat gtc ctc aaa gtt tta cga	768
Met Asn Asn Ile Ser Asn Asn Ser Glu Asp Val Leu Lys Val Leu Arg	
245 250 255	
ttt tta gaa tac ggg atc aac agc ttg tta tac caa gtt gat ttc agg	816
Phe Leu Glu Tyr Gly Ile Asn Ser Leu Leu Tyr Gln Val Asp Phe Arg	
260 265 270	
cgc aat tac tcg gtt tat ttc aac tac act tat att ttt taagcgatag	865
Arg Asn Tyr Ser Val Tyr Phe Asn Tyr Thr Tyr Ile Phe	
275 280 285	
cgtttaaagc gttcttaatt gagcgatttc gtctctcaaaa cgcattcgctt cttcaaaatc	925
caaattcttc gtgcattctc gca	948

<210> 138
 <211> 285
 <212> PRT
 <213> Helicobacter pylori

<400> 138
 Lys Ile Glu Val Leu Arg Gly Phe Leu Lys Arg Ala Leu Tyr Leu Ile
 1 5 10 15
 Leu Gly Leu Phe Tyr Thr Leu Asn Ala Glu Ser Phe Lys Asp Val Leu
 20 25 30
 Thr Lys Val Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile
 35 40 45

60										65					70					
ctt	gcg	gtt	gtc	cat	ccg	gca	gca	ggc	aat	att	ggt	gga	ggc	ggt	ttt	295				
Leu	Ala	Val	Val	His	Pro	Ala	Ala	Gly	Asn	Ile	Gly	Gly	Gly	Gly	Phe					
			75					80					85							
gcg	gtt	atc	cat	ttg	gct	aat	ggt	gaa	aat	gtt	gcg	tta	gat	ttt	aga	343				
Ala	Val	Ile	His	Leu	Ala	Asn	Gly	Glu	Asn	Val	Ala	Leu	Asp	Phe	Arg					
		90					95					100								
gaa	aaa	gcc	ccc	tta	aaa	gcc	act	aaa	aac	atg	ttt	tta	gac	aag	caa	391				
Glu	Lys	Ala	Pro	Leu	Lys	Ala	Thr	Lys	Asn	Met	Phe	Leu	Asp	Lys	Gln					
	105					110					115									
ggc	aat	gta	gtc	cct	aaa	ctc	agc	gaa	gat	ggc	tat	ttg	gcg	gcc	ggg	439				
Gly	Asn	Val	Val	Pro	Lys	Leu	Ser	Glu	Asp	Gly	Tyr	Leu	Ala	Ala	Gly					
120					125					130					135					
gtt	cct	gga	acg	gtg	gca	ggc	atg	gaa	gcg	atg	ctg	aaa	aaa	tac	ggc	487				
Val	Pro	Gly	Thr	Val	Ala	Gly	Met	Glu	Ala	Met	Leu	Lys	Lys	Tyr	Gly					
				140					145					150						
act	aaa	aaa	cta	tcg	caa	ctc	att	gat	cct	gcc	att	aaa	ttg	gct	gaa	535				
Thr	Lys	Lys	Leu	Ser	Gln	Leu	Ile	Asp	Pro	Ala	Ile	Lys	Leu	Ala	Glu					
			155					160					165							
aat	ggt	tat	gcg	att	tca	caa	aga	caa	gca	gaa	acc	cta	aag	gaa	gca	583				
Asn	Gly	Tyr	Ala	Ile	Ser	Gln	Arg	Gln	Ala	Glu	Thr	Leu	Lys	Glu	Ala					
		170					175					180								
agg	gag	cgg	ttt	tta	aaa	tac	agt	tct	agc	aaa	aag	tat	ttt	ttt	aaa	631				
Arg	Glu	Arg	Phe	Leu	Lys	Tyr	Ser	Ser	Ser	Lys	Lys	Tyr	Phe	Phe	Lys					
	185					190					195									
aaa	ggc	cat	ctt	gat	tat	caa	gaa	ggg	gat	ttg	ttt	gtc	caa	aaa	gat	679				
Lys	Gly	His	Leu	Asp	Tyr	Gln	Glu	Gly	Asp	Leu	Phe	Val	Gln	Lys	Asp					
200					205					210					215					
tta	gcc	aag	act	ttg	aat	caa	atc	aaa	acg	cta	ggc	gct	aaa	ggc	ttt	727				
Leu	Ala	Lys	Thr	Leu	Asn	Gln	Ile	Lys	Thr	Leu	Gly	Ala	Lys	Gly	Phe					
				220					225					230						
tat	caa	ggg	caa	gtc	gct	gag	ctt	att	gag	aaa	gac	atg	aaa	aaa	aat	775				
Tyr	Gln	Gly	Gln	Val	Ala	Glu	Leu	Ile	Glu	Lys	Asp	Met	Lys	Lys	Asn					
			235					240					245							
gga	ggg	att	atc	act	aaa	gaa	gat	tta	gcc	agt	tac	aat	gtg	aaa	tgg	823				
Gly	Gly	Ile	Ile	Thr	Lys	Glu	Asp	Leu	Ala	Ser	Tyr	Asn	Val	Lys	Trp					
		250					255					260								
cgc	aaa	ccc	gtg	gta	ggg	agt	tat	cgt	ggg	tat	aag	atc	att	tct	atg	871				
Arg	Lys	Pro	Val	Val	Gly	Ser	Tyr	Arg	Gly	Tyr	Lys	Ile	Ile	Ser	Met					
	265					270					275									
tcg	ccg	cca	agt	tcg	gga	ggc	acg	cat	ttg	atc	cag	att	tta	aat	gtc	919				
Ser	Pro	Pro	Ser	Ser	Gly	Gly	Thr	His	Leu	Ile	Gln	Ile	Leu	Asn	Val					
280					285					290					295					
atg	gaa	aat	gcg	gat	tta	agc	gcc	ctt	ggg	tat	ggg	gct	tct	aag	aat	967				

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Met	Glu	Asn	Ala	Asp	Leu	Ser	Ala	Leu	Gly	Tyr	Gly	Ala	Ser	Lys	Asn		
				300					305					310			
atc	cat	atc	gct	gcc	gaa	gcg	atg	cgt	cag	gct	tat	gcg	gat	aga	tcg		1015
Ile	His	Ile	Ala	Ala	Glu	Ala	Met	Arg	Gln	Ala	Tyr	Ala	Asp	Arg	Ser		
			315					320					325				
gtt	tat	atg	gga	gac	gct	gat	ttt	gtt	tcg	gtg	ccg	gtg	gat	aaa	ttg		1063
Val	Tyr	Met	Gly	Asp	Ala	Asp	Phe	Val	Ser	Val	Pro	Val	Asp	Lys	Leu		
		330					335					340					
att	aat	aaa	gcg	tat	gcc	aaa	aag	att	ttt	gac	act	atc	cag	cca	gat		1111
Ile	Asn	Lys	Ala	Tyr	Ala	Lys	Lys	Ile	Phe	Asp	Thr	Ile	Gln	Pro	Asp		
	345					350				355							
acg	gtt	acg	cca	agc	tct	caa	atc	aaa	cca	gga	atg	ggg	cag	ttg	cat		1159
Thr	Val	Thr	Pro	Ser	Ser	Gln	Ile	Lys	Pro	Gly	Met	Gly	Gln	Leu	His		
	360				365					370					375		
gag	ggg	agc	aat	acc	acg	cat	tat	tct	gta	gcg	gac	agg	tgg	ggg	aat		1207
Glu	Gly	Ser	Asn	Thr	Thr	His	Tyr	Ser	Val	Ala	Asp	Arg	Trp	Gly	Asn		
			380						385					390			
gca	gtc	agc	gtt	act	tac	acc	att	aac	gct	tct	tat	gga	agc	gct	gcc		1255
Ala	Val	Ser	Val	Thr	Tyr	Thr	Ile	Asn	Ala	Ser	Tyr	Gly	Ser	Ala	Ala		
			395					400					405				
agt	att	gat	ggg	gca	gga	ttt	tta	ttg	aac	aat	gaa	atg	gat	gat	ttt		1303
Ser	Ile	Asp	Gly	Ala	Gly	Phe	Leu	Leu	Asn	Asn	Glu	Met	Asp	Asp	Phe		
		410				415						420					
tcc	atc	aag	cca	ggg	aat	ccc	aat	ctc	tat	ggt	tta	gta	ggg	ggc	gat		1351
Ser	Ile	Lys	Pro	Gly	Asn	Pro	Asn	Leu	Tyr	Gly	Leu	Val	Gly	Gly	Asp		
		425				430					435						
gcg	aat	gcg	att	gaa	gcc	aat	aag	cgc	cct	tta	agc	tcc	atg	tcg	cct		1399
Ala	Asn	Ala	Ile	Glu	Ala	Asn	Lys	Arg	Pro	Leu	Ser	Ser	Met	Ser	Pro		
	440				445				450						455		
acg	att	gtg	ttg	aaa	aac	aat	aag	gtt	ttt	ttg	gtg	gtg	gga	agc	cct		1447
Thr	Ile	Val	Leu	Lys	Asn	Asn	Lys	Val	Phe	Leu	Val	Val	Gly	Ser	Pro		
			460					465						470			
gga	ggg	tct	agg	att	atc	act	acg	gtg	ctg	caa	gtg	att	tct	aat	gtc		1495
Gly	Gly	Ser	Arg	Ile	Ile	Thr	Thr	Val	Leu	Gln	Val	Ile	Ser	Asn	Val		
			475					480					485				
att	gat	tat	aat	atg	aat	att	tct	gaa	gcg	gtt	tca	gcc	cca	aga	ttt		1543
Ile	Asp	Tyr	Asn	Met	Asn	Ile	Ser	Glu	Ala	Val	Ser	Ala	Pro	Arg	Phe		
		490					495					500					
cac	atg	caa	tgg	ctc	cct	gat	gaa	tta	agg	att	gaa	aag	ttt	ggc	atg		1591
His	Met	Gln	Trp	Leu	Pro	Asp	Glu	Leu	Arg	Ile	Glu	Lys	Phe	Gly	Met		
	505					510					515						
ccc	gct	gat	gtg	aaa	gac	aac	ctc	act	aaa	atg	ggc	tat	caa	atc	gtt		1639
Pro	Ala	Asp	Val	Lys	Asp	Asn	Leu	Thr	Lys	Met	Gly	Tyr	Gln	Ile	Val		
	520				525					530					535		

Ser Val Pro Val Asp Lys Leu Ile Asn Lys Ala Tyr Ala Lys Lys Ile
 340 345 350
 Phe Asp Thr Ile Gln Pro Asp Thr Val Thr Pro Ser Ser Gln Ile Lys
 355 360 365
 Pro Gly Met Gly Gln Leu His Glu Gly Ser Asn Thr Thr His Tyr Ser
 370 375 380
 Val Ala Asp Arg Trp Gly Asn Ala Val Ser Val Thr Tyr Thr Ile Asn
 385 390 395 400
 Ala Ser Tyr Gly Ser Ala Ala Ser Ile Asp Gly Ala Gly Phe Leu Leu
 405 410 415
 Asn Asn Glu Met Asp Asp Phe Ser Ile Lys Pro Gly Asn Pro Asn Leu
 420 425 430
 Tyr Gly Leu Val Gly Gly Asp Ala Asn Ala Ile Glu Ala Asn Lys Arg
 435 440 445
 Pro Leu Ser Ser Met Ser Pro Thr Ile Val Leu Lys Asn Asn Lys Val
 450 455 460
 Phe Leu Val Val Gly Ser Pro Gly Gly Ser Arg Ile Ile Thr Thr Val
 465 470 475 480
 Leu Gln Val Ile Ser Asn Val Ile Asp Tyr Asn Met Asn Ile Ser Glu
 485 490 495
 Ala Val Ser Ala Pro Arg Phe His Met Gln Trp Leu Pro Asp Glu Leu
 500 505 510
 Arg Ile Glu Lys Phe Gly Met Pro Ala Asp Val Lys Asp Asn Leu Thr
 515 520 525
 Lys Met Gly Tyr Gln Ile Val Thr Lys Pro Val Met Gly Asp Val Asn
 530 535 540
 Ala Ile Gln Val Leu Pro Lys Thr Lys Gly Ser Val Phe Tyr Gly Ser
 545 550 555 560
 Thr Asp Pro Arg Lys Glu Phe
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 <213> Helicobacter pylori
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 aggagaaaca ccacc atg caa aac cat gat tta gag tca atc aaa caa gcc 111
 Met Gln Asn His Asp Leu Glu Ser Ile Lys Gln Ala
 1 5 10
 gct ttg att gaa tat gaa gtg aga gaa caa ggc tct agt att gtg cta 159
 Ala Leu Ile Glu Tyr Glu Val Arg Glu Gln Gly Ser Ser Ile Val Leu
 15 20 25
 gac agc aat att tcc aaa gag cct tta gag ttt att ata ggc act aat 207
 Asp Ser Asn Ile Ser Lys Glu Pro Leu Glu Phe Ile Ile Gly Thr Asn
 30 35 40
 caa atc ata gca ggg tta gaa aag gcg gta tta aag gct caa att ggc 255
 Gln Ile Ile Ala Gly Leu Glu Lys Ala Val Leu Lys Ala Gln Ile Gly
 45 50 55 60
 gag tgg gaa gag gtt gtc atc gcc cca gag gaa gct tat ggg gtt tat 303

[illegible]

<400> 142

-160-

0 9 9 7 1 0 6 8 0 1

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<221> CDS  
<222> (1)...(336)
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<210> 144
<211> 112
<212> PRT
<213> Helicobacter pylori
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-161-

50		55		60
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65		70		75
Phe Asn Ser Ser Ser Asn Thr Gly Ile Cys Ala Cys Asn Cys Ser Phe				80
		85		90
Ser Ala Cys Phe Ser Phe Cys Asn Cys Phe Ala Asn Ala Ser Asn Ser				95
	100		105	110

<210> 145
 <211> 1440
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (34)...(1338)

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Met Gly Phe Phe Lys Leu Lys	
1 5	
gaa cac aac act aac att gcc acc gag ttt aga gcg ggt tta acg acc	102
Glu His Asn Thr Asn Ile Ala Thr Glu Phe Arg Ala Gly Leu Thr Thr	
10 15 20	
ttt atc acc atg att tac atc gtg ccc tta aac gct ctt atc ctt tct	150
Phe Ile Thr Met Ile Tyr Ile Val Pro Leu Asn Ala Leu Ile Leu Ser	
25 30 35	
caa gcc aac atg cct tat gaa gcc ctt tta agt gca acg gcc att atc	198
Gln Ala Asn Met Pro Tyr Glu Ala Leu Leu Ser Ala Thr Ala Ile Ile	
40 45 50 55	
act atc tta tcg agc gtg ttt aac gga ttg tgg gca aac acc cct atc	246
Thr Ile Leu Ser Ser Val Phe Asn Gly Leu Trp Ala Asn Thr Pro Ile	
60 65 70	
gct atg agc gtg ggc tta ggg ctg tca gct tat ttt agc ttc ggg ttg	294
Ala Met Ser Val Gly Leu Gly Leu Ser Ala Tyr Phe Ser Phe Gly Leu	
75 80 85	
gtt caa ggg tta aaa ctc cct tgg cag agc gct tta ggc atc gta gcg	342
Val Gln Gly Leu Lys Leu Pro Trp Gln Ser Ala Leu Gly Ile Val Ala	
90 95 100	
ctc tcg gga gcg att ttt gtg att ttg tct ttc act aaa ttt aga agt	390
Leu Ser Gly Ala Ile Phe Val Ile Leu Ser Phe Thr Lys Phe Arg Ser	
105 110 115	
tgg gtc atg cga agc att cct agc gat tta agg cgt gcg gtg agt gcg	438
Trp Val Met Arg Ser Ile Pro Ser Asp Leu Arg Arg Ala Val Ser Ala	
120 125 130 135	
ggg ata ggg gct ttt atc gcg ttt att ggc ctt aaa gaa atg cat atc	486
Gly Ile Gly Ala Phe Ile Ala Phe Ile Gly Leu Lys Glu Met His Ile	
140 145 150	
gtc gtt acc cat aar gct acg ctt gta acc tta ggc gat ttt ggc gat	534

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Val 155	Val	Thr	His	Xaa	Ala	Thr	Leu	Val	Thr	Leu	Gly	Asp	Phe	Gly	Asp	
ccg Pro	cat His	gtg Val	tta Leu	ttg Leu	ggg Gly	gtt Val	gtg Val	ggg Gly	atc Ile	att Ile	cta Leu	act Thr	ttc Phe	gcg Ala	ctc Leu	582
tac Tyr	acg Thr	ctc Leu	aaa Lys	atc Ile	agg Arg	ggg Gly	tct Ser	ttc Phe	att Ile	ata Ile	gcg Ala	gtc Val	tta Leu	atc Ile	act Thr	630
tcc Ser	att Ile	ctc Leu	gca Ala	tgg Trp	gtt Val	tta Leu	aag Lys	cta Leu	gcc Ala	cct Pro	tac Tyr	cct Pro	agc Ser	gag Glu	ttt Phe	678
ttt Phe	tcc Ser	atg Met	ccc Pro	gct Ala	agc Ser	att Ile	ggc Gly	cct Pro	atc Ile	gcc Ala	ttt Phe	caa Gln	tta Leu	gac Asp	ttt Phe	726
aag Lys	ggc Gly	att Ile	ttt Phe	ttt Phe	gat Asp	gcg Ala	agt Ser	ggg Gly	gct Ala	ttc Phe	act Thr	tta Leu	gcg Ala	tta Leu	gtg Val	774
cca Pro	gtt Val	att Ile	atc Ile	act Thr	ttt Phe	ttt Phe	gta Val	acc Thr	gat Asp	ttg Leu	ttt Phe	gat Asp	tct Ser	tta Leu	ggc Gly	822
acg Thr	ctt Leu	gca Ala	ggg Gly	att Ile	ggc Gly	cac His	aag Lys	act Thr	gat Asp	ttt Phe	ttc Phe	aat Asn	gat Asp	gaa Glu	gaa Glu	870
aaa Lys	aac Asn	aag Lys	gaa Glu	ttg Leu	gaa Glu	aag Lys	act Thr	ttg Leu	gaa Glu	gcg Ala	gat Asp	gcg Ala	gtg Val	gct Ala	tct Ser	918
tta Leu	ggg Gly	agc Ser	gcg Ala	gtg Val	gtg Val	ggc Gly	gtt Val	tct Ser	act Thr	acg Thr	acc Thr	gct Ala	ttt Phe	ata Ile	gag Glu	966
agc Ser	gcg Ala	agt Ser	ggg Gly	gtt Val	gaa Glu	gag Glu	ggg Gly	ggc Gly	cgc Arg	aca Thr	ggg Gly	ctt Leu	aca Thr	gcg Ala	gtt Val	1014
ttt Phe	acc Thr	gga Gly	tta Leu	ttt Phe	ttt Phe	gtt Val	tta Leu	acg Thr	ctc Leu	ttt Phe	tgc Cys	ttg Leu	cct Pro	ctt Leu	tta Leu	1062
aaa Lys	gct Ala	att Ile	cct Pro	agc Ser	aat Asn	gcg Ala	att Ile	tat Tyr	ccg Pro	gtg Val	ctg Leu	gtg Val	gta Val	gta Val	ggg Gly	1110
gtt Val	ttg Leu	atg Met	ttt Phe	agc Ser	gtg Val	tta Leu	gag Glu	ggg Gly	gtg Val	aat Asn	ttt Phe	aaa Lys	gac Asp	atg Met	gcc Ala	1158
att Ile	agc Ser	gtt Val	tcc Ser	act Thr	ttt Phe	tta Leu	acc Thr	gtg Val	gtg Val	atg Met	atg Met	ccc Pro	tta Leu	acc Thr	ttc Phe	1206

Thr Thr Thr Ala Phe Ile Glu Ser Ala Ser Gly Val Glu Glu Gly Gly
 305 310 315 320
 Arg Thr Gly Leu Thr Ala Val Phe Thr Gly Leu Phe Phe Val Leu Thr
 325 330 335
 Leu Phe Cys Leu Pro Leu Leu Lys Ala Ile Pro Ser Asn Ala Ile Tyr
 340 345 350
 Pro Val Leu Val Val Val Gly Val Leu Met Phe Ser Val Leu Glu Gly
 355 360 365
 Val Asn Phe Lys Asp Met Ala Ile Ser Val Ser Thr Phe Leu Thr Val
 370 375 380
 Val Met Met Pro Leu Thr Phe Ser Ile Ala Asp Gly Leu Ala Phe Gly
 385 390 395 400
 Phe Leu Ser Tyr Ser Ile Ile Lys Leu Val Gln Lys Asp Phe Lys Ala
 405 410 415
 Leu Asn Ser Gly Ile Ile Ile Leu Cys Ile Ile Ser Val Ser Val Phe
 420 425 430
 Ile Phe Arg
 435

<210> 147
 <211> 843
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (66)...(764)

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 caacc atg acc cct cac atc aac gcc aaa atc ggc gat ttt tat cct caa 110
 Met Thr Pro His Ile Asn Ala Lys Ile Gly Asp Phe Tyr Pro Gln
 1 5 10 15

 tgc ctt tta tgc ggc gat ccc tta agg gtg agc tac att gca aaa aaa 158
 Cys Leu Leu Cys Gly Asp Pro Leu Arg Val Ser Tyr Ile Ala Lys Lys
 20 25 30

 ttc tta caa gac gcc aaa gag atc acg aat gtg cgt aac atg cta ggc 206
 Phe Leu Gln Asp Ala Lys Glu Ile Thr Asn Val Arg Asn Met Leu Gly
 35 40 45

 ttt agc ggg aag tat aag ggt agg ggg att tct tta atg ggg cat ggc 254
 Phe Ser Gly Lys Tyr Lys Gly Arg Gly Ile Ser Leu Met Gly His Gly
 50 55 60

 atg ggc att gcg tca tgc acg att tat gta acc gaa ctc att aaa acc 302
 Met Gly Ile Ala Ser Cys Thr Ile Tyr Val Thr Glu Leu Ile Lys Thr
 65 70 75

 tat cag gtt aaa gag ctt tta agg att ggc act tgc ggg gcg att agc 350
 Tyr Gln Val Lys Glu Leu Leu Arg Ile Gly Thr Cys Gly Ala Ile Ser
 80 85 90 95

 cca aaa gtt ggc ctg aaa gac att atc atg gcg acg ggg gct tca acg 398
 Pro Lys Val Gly Leu Lys Asp Ile Ile Met Ala Thr Gly Ala Ser Thr
 100 105 110

 gat tct aaa acc aat cgg gtg cgt ttt tta aac cac gat ttg agc gca 446

Ser Phe Glu Thr His Ala Phe Asp Leu Met Ala Lys Tyr Asn His Leu
165 170 175
Ala Ile Glu Met Glu Ala Ala Gly Leu Tyr Ala Thr Ala Met Glu Leu
180 185 190
Asn Ala Lys Ala Leu Cys Leu Cys Ser Val Ser Asp His Leu Ile Thr
195 200 205
Lys Glu Ala Leu Ser Pro Lys Glu Arg Val Glu Ser Phe Asp Asn Met
210 215 220
Ile Ile Leu Ala Leu Glu Met Met Ser
225 230

<210> 149
<211> 1440
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (79)...(1407)

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tcttgtaaaa taaccgcg atg ttt aag aaa att ttt cca tta gcg tta gtg 111
Met Phe Lys Lys Ile Phe Pro Leu Ala Leu Val
1 5 10
tca tcg ttg cgg ttt ttg ggg ctt ttt att gtt ttg ccg gtc att agt 159
Ser Ser Leu Arg Phe Leu Gly Leu Phe Ile Val Leu Pro Val Ile Ser
15 20 25
ttg tat gcg gat agt ttc cat tca agc agt ccc tta ctc gtg ggg ttg 207
Leu Tyr Ala Asp Ser Phe His Ser Ser Ser Pro Leu Leu Val Gly Leu
30 35 40
gct gtg ggc gga gcg tat ctt acg caa att gtt ttt caa acc ccc atg 255
Ala Val Gly Gly Ala Tyr Leu Thr Gln Ile Val Phe Gln Thr Pro Met
45 50 55
ggc att ctt agc gat aag ata ggc cgt aaa gtg gtg gtt atg gtg tgc 303
Gly Ile Leu Ser Asp Lys Ile Gly Arg Lys Val Val Val Met Val Cys
60 65 70 75
ttg ctg ttg ttt tta gcc ggc tcg tta gtg tgc ttt ata gcg aat gat 351
Leu Leu Leu Phe Leu Ala Gly Ser Leu Val Cys Phe Ile Ala Asn Asp
80 85 90
att gtt tgg ctc gtt ata ggg cgc ttc att caa ggc atg ggg gct tta 399
Ile Val Trp Leu Val Ile Gly Arg Phe Ile Gln Gly Met Gly Ala Leu
95 100 105
ggg ggg gtt att agt gcg atg gtg gcg gat gaa gtg aaa gaa gaa gag 447
Gly Gly Val Ile Ser Ala Met Val Ala Asp Glu Val Lys Glu Glu Glu
110 115 120
cgc acc aaa gcc atg gcc atc atg gga gcg ttt att ttc att agc ttc 495
Arg Thr Lys Ala Met Ala Ile Met Gly Ala Phe Ile Phe Ile Ser Phe
125 130 135
act ata agc atg gcg att ggc cct ggg gtt gta gcg ttt ttg ggg ggg 543

Thr	Ile	Ser	Met	Ala	Ile	Gly	Pro	Gly	Val	Val	Ala	Phe	Leu	Gly	Gly		
140					145					150					155		
gca	aaa	tgg	ctc	ttt	tta	ctc	acg	gcg	atc	tta	act	tta	ttg	agt	tta	591	
Ala	Lys	Trp	Leu	Phe	Leu	Leu	Thr	Ala	Ile	Leu	Thr	Leu	Leu	Ser	Leu		
				160					165					170			
ttg	atg	ctt	tta	aaa	gtc	aaa	gac	gcc	cct	aaa	att	tct	tac	cag	atc	639	
Leu	Met	Leu	Leu	Lys	Val	Lys	Asp	Ala	Pro	Lys	Ile	Ser	Tyr	Gln	Ile		
				175				180					185				
aaa	aac	ata	aaa	gct	tac	caa	ccc	aac	tct	aaa	gcc	ttg	tat	ctt	ttg	687	
Lys	Asn	Ile	Lys	Ala	Tyr	Gln	Pro	Asn	Ser	Lys	Ala	Leu	Tyr	Leu	Leu		
		190					195					200					
tat	cta	agc	tct	ttt	ttt	gaa	aaa	gcg	ttc	atg	acg	ctt	att	ttt	gtg	735	
Tyr	Leu	Ser	Ser	Phe	Phe	Glu	Lys	Ala	Phe	Met	Thr	Leu	Ile	Phe	Val		
	205					210					215						
ctg	atc	cct	tta	gcc	tta	gtg	aat	gaa	ttt	cat	aaa	gat	gaa	agc	ttt	763	
Leu	Ile	Pro	Leu	Ala	Leu	Val	Asn	Glu	Phe	His	Lys	Asp	Glu	Ser	Phe		
	220				225					230					235		
tta	atc	ttg	gtg	tat	gtg	cct	gga	gcc	tta	tta	ggg	gtc	tta	agc	atg	831	
Leu	Ile	Leu	Val	Tyr	Val	Pro	Gly	Ala	Leu	Leu	Gly	Val	Leu	Ser	Met		
				240					245					250			
gga	ata	gcg	agc	gtt	atg	gct	gaa	aaa	tac	aac	aag	cct	aaa	gga	gtg	879	
Gly	Ile	Ala	Ser	Val	Met	Ala	Glu	Lys	Tyr	Asn	Lys	Pro	Lys	Gly	Val		
			255					260					265				
atg	ctt	tct	ggc	gta	tta	ttg	ttt	att	gtg	agt	tat	ttg	tgc	ttg	ttt	927	
Met	Leu	Ser	Gly	Val	Leu	Leu	Phe	Ile	Val	Ser	Tyr	Leu	Cys	Leu	Phe		
		270					275					280					
tta	gcc	gac	tct	agc	ttt	tta	ggg	aaa	tat	tta	tgg	ctt	ttt	att	gtt	975	
Leu	Ala	Asp	Ser	Ser	Phe	Leu	Gly	Lys	Tyr	Leu	Trp	Leu	Phe	Ile	Val		
	285					290					295						
ggg	gtg	gcg	ttt	ttc	ttt	att	ggt	ttt	gcc	acc	tta	gag	cct	atc	atg	1023	
Gly	Val	Ala	Phe	Phe	Phe	Ile	Gly	Phe	Ala	Thr	Leu	Glu	Pro	Ile	Met		
	300				305					310					315		
caa	tct	tta	gcg	tct	aaa	ttc	gcc	aaa	gtg	cat	gaa	aaa	ggc	aag	gtt	1071	
Gln	Ser	Leu	Ala	Ser	Lys	Phe	Ala	Lys	Val	His	Glu	Lys	Gly	Lys	Val		
				320					325					330			
tta	ggg	caa	ttc	act	act	ttt	ggc	tat	tta	ggg	agc	ttt	gtt	ggg	ggc	1119	
Leu	Gly	Gln	Phe	Thr	Thr	Phe	Gly	Tyr	Leu	Gly	Ser	Phe	Val	Gly	Gly		
			335					340					345				
gtg	agc	ggg	ggg	ttg	agc	tac	cat	cat	tta	ggc	gtt	tct	aac	aca	agc	1167	
Val	Ser	Gly	Gly	Leu	Ser	Tyr	His	His	Leu	Gly	Val	Ser	Asn	Thr	Ser		
		350					355					360					
ttg	atc	gtt	gta	gct	tta	ggg	ctt	att	tgg	ggg	cta	tcg	ctc	ttt	tta	1215	
Leu	Ile	Val	Val	Ala	Leu	Gly	Leu	Ile	Trp	Gly	Leu	Ser	Leu	Phe	Leu		
	365					370					375						

ctc aac aac cct tcc aag caa aaa aat gtc tat ttc ccc tta gac gct 1263
 Leu Asn Asn Pro Ser Lys Gln Lys Asn Val Tyr Phe Pro Leu Asp Ala
 380 385 390 395

tac aat gag gaa caa ttt gaa act tta gag gat aaa atc att gaa tgg 1311
 Tyr Asn Glu Glu Gln Phe Glu Thr Leu Glu Asp Lys Ile Ile Glu Trp
 400 405 410

tat gtt aat att agc gaa gaa atc att att gtg aaa tat aat tcc gat 1359
 Tyr Val Asn Ile Ser Glu Glu Ile Ile Ile Val Lys Tyr Asn Ser Asp
 415 420 425

cac att agc gaa gaa gaa atc att cac tta gcg caa aac ttt aga aaa 1407
 His Ile Ser Glu Glu Glu Ile Ile His Leu Ala Gln Asn Phe Arg Lys
 430 435 440

taaaacaatt aaggatcaaaa aatggcctat gaa 1440

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 <213> Helicobacter pylori

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 Phe His Ser Ser Pro Leu Leu Val Gly Leu Ala Val Gly Gly Ala
 35 40 45
 Tyr Leu Thr Gln Ile Val Phe Gln Thr Pro Met Gly Ile Leu Ser Asp
 50 55 60
 Lys Ile Gly Arg Lys Val Val Val Met Val Cys Leu Leu Leu Phe Leu
 65 70 75 80
 Ala Gly Ser Leu Val Cys Phe Ile Ala Asn Asp Ile Val Trp Leu Val
 85 90 95
 Ile Gly Arg Phe Ile Gln Gly Met Gly Ala Leu Gly Gly Val Ile Ser
 100 105 110
 Ala Met Val Ala Asp Glu Val Lys Glu Glu Glu Arg Thr Lys Ala Met
 115 120 125
 Ala Ile Met Gly Ala Phe Ile Phe Ile Ser Phe Thr Ile Ser Met Ala
 130 135 140
 Ile Gly Pro Gly Val Val Ala Phe Leu Gly Gly Ala Lys Trp Leu Phe
 145 150 155 160
 Leu Leu Thr Ala Ile Leu Thr Leu Leu Ser Leu Leu Met Leu Leu Lys
 165 170 175
 Val Lys Asp Ala Pro Lys Ile Ser Tyr Gln Ile Lys Asn Ile Lys Ala
 180 185 190
 Tyr Gln Pro Asn Ser Lys Ala Leu Tyr Leu Leu Tyr Leu Ser Ser Phe
 195 200 205
 Phe Glu Lys Ala Phe Met Thr Leu Ile Phe Val Leu Ile Pro Leu Ala
 210 215 220
 Leu Val Asn Glu Phe His Lys Asp Glu Ser Phe Leu Ile Leu Val Tyr
 225 230 235 240
 Val Pro Gly Ala Leu Leu Gly Val Leu Ser Met Gly Ile Ala Ser Val
 245 250 255
 Met Ala Glu Lys Tyr Asn Lys Pro Lys Gly Val Met Leu Ser Gly Val
 260 265 270
 Leu Leu Phe Ile Val Ser Tyr Leu Cys Leu Phe Leu Ala Asp Ser Ser

	90				95				100								
ctt	aat	tta	gag	cct	att	ttt	atg	gtg	att	ttc	cct	att	att	agt	ttg	448	
Leu	Asn	Leu	Glu	Pro	Ile	Phe	Met	Val	Ile	Phe	Pro	Ile	Ile	Ser	Leu		
105					110					115					120		
ggc	atg	atc	atg	act	tta	gtc	aaa	gat	tat	cgt	aaa	gag	att	ttg	tgg	496	
Gly	Met	Ile	Met	Thr	Leu	Val	Lys	Asp	Tyr	Arg	Lys	Glu	Ile	Leu	Trp		
				125					130					135			
ctt	gat	ttg	gtt	ttg	aaa	gtg	ggc	gtt	att	ggg	gaa	ttg	tta	agc	att	544	
Leu	Asp	Leu	Val	Leu	Lys	Val	Gly	Val	Ile	Gly	Glu	Leu	Leu	Ser	Ile		
			140					145					150				
ttt	ggt	ttg	gtg	gtc	gtg	gat	ggg	gtg	tat	tcg	cat	ggt	ttg	ggc	atg	592	
Phe	Gly	Leu	Val	Val	Val	Asp	Gly	Val	Tyr	Ser	His	Gly	Leu	Gly	Met		
		155					160					165					
gat	ttg	att	aaa	gat	tta	ggc	att	ctc	att	gtt	ttt	tta	atc	tta	att	640	
Asp	Leu	Ile	Lys	Asp	Leu	Gly	Ile	Leu	Ile	Val	Phe	Leu	Ile	Leu	Ile		
	170					175					180						
atc	gtg	gcg	ttt	caa	atc	ttt	aag	act	ttg	ttt	tgg	tgg	ttc	ccg	cat	688	
Ile	Val	Ala	Phe	Gln	Ile	Phe	Lys	Thr	Leu	Phe	Trp	Trp	Phe	Pro	His		
185					190					195					200		
tta	aag	ctt	ttt	gtg	atg	cct	aaa	agc	agt	cag	ttt	aac	caa	gat	gtg	736	
Leu	Lys	Leu	Phe	Val	Met	Pro	Lys	Ser	Ser	Gln	Phe	Asn	Gln	Asp	Val		
				205					210					215			
cgt	ttt	tcg	ctc	atg	ctc	ttt	ttt	tcc	tta	gtt	gcg	atc	gtg	gtg	tgg	784	
Arg	Phe	Ser	Leu	Met	Leu	Phe	Phe	Ser	Leu	Val	Ala	Ile	Val	Val	Trp		
			220					225					230				
ctc	aaa	ata	gaa	atg	gtt	tta	ggg	gcg	ttt	cta	gca	ggg	tta	gtc	gtt	832	
Leu	Lys	Ile	Glu	Met	Val	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Leu	Val	Val		
		235					240					245					
tct	act	ttt	ttc	cct	cat	aaa	tca	gaa	ttg	atc	cac	aag	ctc	aat	gat	880	
Ser	Thr	Phe	Phe	Pro	His	Lys	Ser	Glu	Leu	Ile	His	Lys	Leu	Asn	Asp		
	250					255					260						
gtg	ggt	ttt	ggg	ttt	ttt	gtg	cct	ttg	ttt	ttc	atc	cat	gta	ggc	tct	928	
Val	Gly	Phe	Gly	Phe	Phe	Val	Pro	Leu	Phe	Phe	Ile	His	Val	Gly	Ser		
265					270					275					280		
act	tta	gac	tta	aaa	tta	gtg	ttt	tta	aac	ccg	cat	ttg	att	ctc	caa	976	
Thr	Leu	Asp	Leu	Lys	Leu	Val	Phe	Leu	Asn	Pro	His	Leu	Ile	Leu	Gln		
				285					290					295			
ggg	ata	ttg	att	gtc	ata	gcg	atg	ttg	agt	ttg	cac	ttg	atc	act	tca	1024	
Gly	Ile	Leu	Ile	Val	Ile	Ala	Met	Leu	Ser	Leu	His	Leu	Ile	Thr	Ser		
	</																

Phe Ala Leu Gly Ala Ser Met Pro Leu Thr Phe Leu Val Thr Thr Ala
 330 335 340

gca gta ggc tta aaa gcg caa gcg atc tca caa aac acc tac tac gca 1168
 Ala Val Gly Leu Lys Ala Gln Ala Ile Ser Gln Asn Thr Tyr Tyr Ala
 345 350 355 360

ttg ctc atg gcg gct att ttt gaa ggg gta tta ttc acg att gcg atc 1216
 Leu Leu Met Ala Ala Ile Phe Glu Gly Val Leu Phe Thr Ile Ala Ile
 365 370 375

aaa ata ctc aac aaa aaa gct tgaatgaaag cttaagcgctc taaatattta 1267
 Lys Ile Leu Asn Lys Lys Ala
 380

gcgtcgctaa agctgttcgc ttgaacatta ttgaacgcat tctctaagct atcaaagaaa 1327
 cgagggtgca agttttgcat ttcttttaag aaa 1360

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 <213> Helicobacter pylori

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Met Ala Pro Tyr Met Ser Arg Ile Ser Arg Leu Pro Ile Thr Val Val
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Glu Ile Leu Phe Gly Ser Val Gly Ala Tyr Val Gly Phe Ile Glu Pro
 35 40 45

Thr Lys Gly Phe Glu Ile Met Ser Glu Ile Gly Phe Leu Phe Leu Met
 50 55 60

Phe Leu Cys Gly Leu Glu Val Glu Ile Tyr Leu Phe Lys Lys Leu Gly
 65 70 75 80

Val Ser Leu Leu Lys Arg Ile Phe Ala Tyr Leu Leu Ile Leu Tyr Thr
 85 90 95

Leu Ser Phe Ile Leu Thr Phe Ser Leu Asn Leu Glu Pro Ile Phe Met
 100 105 110

Val Ile Phe Pro Ile Ile Ser Leu Gly Met Ile Met Thr Leu Val Lys
 115 120 125

Asp Tyr Arg Lys Glu Ile Leu Trp Leu Asp Leu Val Leu Lys Val Gly
 130 135 140

Val Ile Gly Glu Leu Leu Ser Ile Phe Gly Leu Val Val Val Asp Gly
 145 150 155 160

Val Tyr Ser His Gly Leu Gly Met Asp Leu Ile Lys Asp Leu Gly Ile
 165 170 175

Leu Ile Val Phe Leu Ile Leu Ile Ile Val Ala Phe Gln Ile Phe Lys
 180 185 190

Thr Leu Phe Trp Trp Phe Pro His Leu Lys Leu Phe Val Met Pro Lys
 195 200 205

Ser Ser Gln Phe Asn Gln Asp Val Arg Phe Ser Leu Met Leu Phe Phe
 210 215 220

Ser Leu Val Ala Ile Val Val Trp Leu Lys Ile Glu Met Val Leu Gly
 225 230 235 240

Ala Phe Leu Ala Gly Leu Val Val Ser Thr Phe Phe Pro His Lys Ser
 245 250 255

Glu Leu Ile His Lys Leu Asn Asp Val Gly Phe Gly Phe Phe Val Pro
 260 265 270

Leu Phe Phe Ile His Val Gly Ser Thr Leu Asp Leu Lys Leu Val Phe

275	280	285
Leu Asn Pro His Leu Ile	Leu Gln Gly Ile Leu Ile	Val Ile Ala Met
290	295	300
Leu Ser Leu His Leu Ile	Thr Ser Thr Leu Leu Trp	Arg Lys Tyr Phe
305	310	315
Lys Glu Ala Lys His Leu Phe	Ser Phe Ala Leu Gly	Ala Ser Met Pro
325	330	335
Leu Thr Phe Leu Val Thr Thr	Ala Ala Val Gly Leu Lys	Ala Gln Ala
340	345	350
Ile Ser Gln Asn Thr Tyr Tyr	Ala Leu Leu Met Ala Ala	Ile Phe Glu
355	360	365
Gly Val Leu Phe Thr Ile Ala	Ile Lys Ile Leu Asn Lys	Lys Ala
370	375	380

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 <213> Helicobacter pylori

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gcgaatgccca ttacaaatat aatcagatca gttggtgggt tttttacaaa gatt atg	117
	Met
	1
aag aga gtt aga gaa ctt gta aaa aaa cat ccc gag aaa agc agt gtg	165
Lys Arg Val Arg Glu Leu Val Lys Lys His Pro Glu Lys Ser Ser Val	
5 10 15	
gca tta gta gta tta acc cat gct gca tgc aag aaa gcg aaa gaa ttg	213
Ala Leu Val Val Leu Thr His Ala Ala Cys Lys Lys Ala Lys Glu Leu	
20 25 30	
gac gat aaa gtc cag gat aaa tcc aaa caa gct gaa aaa gaa aat caa	261
Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu Asn Gln	
35 40 45	
atc aat tgg tgg aaa tat tca gga tta aca ata gcg aca agt tta tta	309
Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser Leu Leu	
50 55 60 65	
tta gcc gct tgt agt gtt ggt gat att gat aaa cag ata gag tta gaa	357
Leu Ala Ala Cys Ser Val Gly Asp Ile Asp Lys Gln Ile Glu Leu Glu	
70 75 80	
caa gaa aaa aag gaa gct gaa aac gct agg gat aga gcg aac aag agt	405
Gln Glu Lys Lys Glu Ala Glu Asn Ala Arg Asp Arg Ala Asn Lys Ser	
85 90 95	
ggg ata gaa ctg gaa cag gaa aaa caa aag acc att aaa gaa caa aaa	453
Gly Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Ile Lys Glu Gln Lys	
100 105 110	
gat tta gtt aaa aaa gca gaa caa aat tgc caa gaa aat cat ggc caa	501
Asp Leu Val Lys Lys Ala Glu Gln Asn Cys Gln Glu Asn His Gly Gln	

115					120					125										
ttc	ttt	atg	aaa	aaa	tta	gga	att	aag	ggt	ggc	att	gct	ata	gaa	gta	549				
Phe	Phe	Met	Lys	Lys	Leu	Gly	Ile	Lys	Gly	Gly	Ile	Ala	Ile	Glu	Val					
130					135					140					145					
gaa	gct	gaa	tgc	aaa	acc	cct	aaa	cct	gca	aaa	acc	aat	caa	acc	cct	597				
Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr	Asn	Gln	Thr	Pro					
				150					155					160						
atc	cag	cca	aaa	cac	ctc	ccc	aac	tct	aaa	caa	ccc	cac	tct	caa	aga	645				
Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro	His	Ser	Gln	Arg					
			165				170					175								
gga	tca	aaa	gcg	caa	gag	ctt	atc	gct	tat	ttg	caa	aaa	gag	tta	gaa	693				
Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr	Leu	Gln	Lys	Glu	Leu	Glu					
		180				185					190									
tct	ctg	ccc	tat	tca	caa	aaa	gct	atc	gct	aaa	caa	gtg	aat	ttt	tac	741				
Ser	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala	Lys	Gln	Val	Asn	Phe	Tyr					
	195					200				205										
agg	cca	agt	tct	gtc	gct	tat	tta	gaa	cta	gac	cct	aga	gat	ttt	aag	789				
Arg	Pro	Ser	Ser	Val	Ala	Tyr	Leu	Glu	Leu	Asp	Pro	Arg	Asp	Phe	Lys					
210				215					220						225					
gtt	aca	gaa	gaa	tgg	caa	aaa	gaa	aat	cta	aaa	ata	cgc	tct	aaa	gct	837				
Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	Lys	Ile	Arg	Ser	Lys	Ala					
				230				235						240						
caa	gct	aaa	atg	ctt	gga	aat	gag	aaa	ccc	aca	agc	cca	cct	ttc	aac	885				
Gln	Ala	Lys	Met	Leu	Gly	Asn	Glu	Lys	Pro	Thr	Ser	Pro	Pro	Phe	Asn					
			245				250					255								
ctc	tca	aag	cct	ttt	gtt	cgt	tca	aaa	aat	att	tgc	tgat	gtta	aat		931				
Leu	Ser	Lys	Pro	Phe	Val	Arg	Ser	Lys	Asn	Ile	Cys									
		260				265														
aaagaaatag		aagcagttgc		taatactgaa		aagaaagcag		aaaaagmggg		ttaatggttat							991			
agtaaaaagga		tgtaggcata		agaaaataag		aac												1024		

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<210> 154
<211> 269
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<213> Helicobacter pylori
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Val	Ala	Leu	Val	Val	Leu	Thr	His	Ala	Ala	Cys	Lys	Lys	Ala	Lys	Glu
			20					25					30		
Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu	Asn
		35				40						45			
Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Thr	Ser	Leu
	50					55					60				
Leu	Leu	Ala	Ala	Cys	Ser	Val	Gly	Asp	Ile	Asp	Lys	Gln	Ile	Glu	Leu
65				70					75					80	
Glu	Gln	Glu	Lys	Lys	Glu	Ala	Glu	Asn	Ala	Arg	Asp	Arg	Ala	Asn	Lys
				85					90					95	

85	90	95	
ccg ttg gtg gaa atg ttt ggc tat tct acg gat tta cga tca gcc acc			392
Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr			
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caa ggg cgt ggg act tac tct atg gag ttt gat cat tat ggc gaa gtg			440
Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val			
115	120	125	130
cct agc aat atc gct aag gaa att gta gaa aag cgc aaa ggc			482
Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly			
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tgatttaatt ataacgctct cttattttta gggggtgtta taggtgctgt tta			535
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Thr Leu Tyr Asp Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala			
20 25 30			
Phe Lys Ile Ala Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala			
35 40 45			
Asn Pro Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro			
50 55 60			
Glu Glu Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly			
65 70 75 80			
Gln Ile Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala			
85 90 95			
Phe Val Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser			
100 105 110			
Ala Thr Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly			
115 120 125			
Glu Val Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly			
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		1	
tta ggc aac ccg cat tca tcc att ttg aga tta ggc cca acc aca atc			104
Leu Gly Asn Pro His Ser Ser Ile Leu Arg Leu Gly Pro Thr Thr Ile			
5 10 15			

acg Thr	ctt Leu 20	ctg Leu	cct Pro	gaa Glu	aaa Lys	tcc Ser 25	acg Thr	cgc Arg	tta Leu	cct Pro	aaa Lys 30	agg Arg	ttt Phe	tgc Cys	ctg Leu	152
aaa Lys 35	cgc Arg	ccc Pro	tgc Cys	ttg Leu	cct Pro 40	tta Leu	atg Met	att Ile	tca Ser	ctg Leu 45	agc Ser	gat Asp	ttt Phe	aaa Lys	ggg Gly 50	200
cgt Arg	ttg Leu	tta Leu	gcc Ala	cct Pro 55	tta Leu	acc Thr	gca Ala	tta Leu	gtg Val 60	ctg Leu	cgg Arg	ccg Pro	tta Leu	tca Ser 65	aaa Lys	248
agc Ser	aca Thr	tcc Ser	acg Thr 70	gct Ala	tct Ser	tgc Cys	aac Asn	atc Ile 75	ctt Leu	ttt Phe	tca Ser	ttg Leu	cgc Arg 80	aca Thr	atg Met	296
att Ile	tct Ser	ggc Gly 85	gct Ala	cca Pro	agc Ser	tcc Ser 90	att Ile	aag Lys	cgt Arg	ttc Phe	aag Lys 95	cgt Arg 95	tgg Trp	tta Leu	cga Arg	344
ttg Leu 100	atg Met	aca Thr	cga Arg	cga Arg	tac Tyr	aat Asn 105	tca Ser	ttc Phe	aca Thr	tcg Ser	ctg Leu 110	act Thr	gca Ala	aac Asn	ttc Phe	392
ccg Pro 115	cca Pro	tct Ser	agc Ser	gcg Ala	act Thr 120	aaa Lys	ggc Gly	ctt Leu	aaa Lys	tcc Ser 125	ggg Gly	ggc Gly	aat Asn	acc Thr	ggt Gly 130	440
aaa Lys	acc Thr	gtg Val	agc Ser	atc Ile 135	atc Ile	cat His	tca Ser	ggc Gly	cta Leu 140	tta Leu	cca Pro	gaa Glu	ttt Phe	aaa Lys 145	aag Lys	488
ctt Leu	tct Ser	acc Thr 150	act Thr	ttc Phe	aaa Lys	cgc Arg	tta Leu	atg Met 155	agt Ser	ttt Phe	ttc Phe	ttt Phe	ttc Phe 160	gca Ala	tca Ser	536
gaa Glu	ttg Leu 165	gtg Val	tct Ser	ttc Phe	act Thr	tct Ser	tct Ser 170	ttc Phe	aaa Lys	ctc Leu	tgc Cys	aat Asn 175	aag Lys	gtg Val	atc Ile	584
aaa Lys	tca Ser 180	att Ile	tct Ser	tct Ser	aac Asn	aaa Lys 185	tcc Ser	ttg Leu	atc Ile	gct Ala	tca Ser 190	ccg Pro	ccc Pro	att Ile	tgc Cys	632
gct Ala 195	aca Thr	aag Lys	ccc Pro	ctg Leu	tct Ser 200	tcg Ser	tat Tyr	ctt Leu	cgt Arg	gag Glu 205	ata Ile	ttt Phe	tgata	ctgct		681
cttcattcaa	aatatc	gttat	ttcatc	caaaa	gcttagt	gcc	ttcattg	tca	taagc	ggct						740

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<210> 158
<211> 207
<212> PRT
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35						40				45						
gtg Val	ggt Val	ttt Phe	agc Ser	atg Met	cct Pro	gag Glu	att Ile	ggg Gly	gtt Val	gtg Val	ggt Gly	gct Ala	aat Asn	tct Ser	aaa Lys	249
50						55				60						
gat Asp	gat Asp	gaa Glu	tcc Ser	ttt Phe	ttt Phe	tca Ser	tgc Cys	gca Ala	ggg Gly	gtt Val	tta Leu	gcg Ala	cgc Arg	cat His	tac Tyr	297
70						75				80						
aac Asn	gaa Glu	ttt Phe	ttt Phe	tct Ser	aac Asn	tca Ser	agg Arg	gcg Ala	gat Asp	ttt Phe	agc Ser	ttg Leu	agc Ser	gct Ala	tat Tyr	345
85						90				95						
ttg Leu	aaa Lys	gag Glu	cgt Arg	ggc Gly	gtt Val	tta Leu	ggg Gly	gtt Val	tgt Cys	ggc Gly	gtt Val	gat Asp	act Thr	agg Arg	agt Ser	393
100						105				110						
ttg Leu	att Ile	aaa Lys	acc Thr	tta Leu	cgc Arg	cat His	cat His	ggg Gly	tgc Cys	tta Leu	atg Met	atg Met	gtc Val	gct Ala	tcc Ser	441
115						120				125						
acg Thr	ata Ile	gag Glu	cat His	gac Asp	aaa Lys	aac Asn	aag Lys	ctt Leu	gaa Glu	gaa Glu	att Ile	tta Leu	aaa Lys	aac Asn	gct Ala	489
130						135				140						
cct Pro	aaa Lys	att Ile	tct Ser	cac His	tcc Ser	ccc Pro	cta Leu	gtg Val	tct Ser	agc Ser	gtt Val	tct Ser	acg Thr	cca Pro	aaa Lys	537
150						155				160						
ata Ile	acc Thr	acg Thr	cac His	cag Gln	cgt Arg	gcg Ala	act Thr	ttt Phe	gat Asp	ttc Phe	aaa Lys	acc Thr	cta Leu	gat Asp	tac Tyr	585
165						170				175						
aag Lys	cct Pro	ttt Phe	gat Asp	gaa Glu	aaa Lys	acc Thr	tct Ser	cat His	aaa Lys	att Ile	atc Ile	gcg Ala	gtg Val	tta Leu	gac Asp	633
180						185				190						
ttt Phe	ggg Gly	gct Ala	aag Lys	ggc Gly	aat Asn	att Ile	tta Leu	aac Asn	gag Glu	ctt Leu	caa Gln	aat Asn	gtg Val	ggg Gly	tta Leu	681
195						200				205						
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210						215				220						
gcc Ala	tat Tyr	gaa Glu	aaa Lys	aaa Lys	gaa Glu	att Ile	agc Ser	ggg Gly	att Ile	ttc Phe	ctc Leu	tct Ser	aac Asn	ggg Gly	ccg Pro	777
230						235				240						
ggc Gly	gat Asp	cct Pro	tta Leu	agc Ser	ttg Leu	cag Gln	caa Gln	gaa Glu	att Ile	ggc Gly	gaa Glu	atc Ile	aaa Lys	caa Gln	ctc Leu	825
245						250				255						
att Leu	aac Lys	gct Val	aaa Lys	atc Tyr	ccc Pro	atg Leu	ctt Leu	ggc Glu	att Ile	tgc Val	tta Leu	ggg Glu	cat Tyr	caa Gln	ttg Leu	873

0005913 062901

Ile Asn Ala Lys Ile Pro Met Leu Gly Ile Cys Leu Gly His Gln Leu	
260 265 270	
ctc tct atc gct caa ggc tac cct act tac aag ctc aaa ttt ggt cat	921
Leu Ser Ile Ala Gln Gly Tyr Pro Thr Tyr Lys Leu Lys Phe Gly His	
275 280 285	
cat ggg agc aac cac ccc gtt aaa aac cta aaa aca aac gcc gta gaa	969
His Gly Ser Asn His Pro Val Lys Asn Leu Lys Thr Asn Ala Val Glu	
290 295 300 305	
atc acc gcg caa aac cac aac tat tgc gtc cct gaa gac att gaa gaa	1017
Ile Thr Ala Gln Asn His Asn Tyr Cys Val Pro Glu Asp Ile Glu Glu	
310 315 320	
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Ile Ala Ile Ile Thr His Arg Asn Leu Phe Asp Asn Thr Ile Glu Gly	
325 330 335	
gtg cgt tat aaa aac gct ccc att atc tct gtc cag cac cac cca gaa	1113
Val Arg Tyr Lys Asn Ala Pro Ile Ile Ser Val Gln His His Pro Glu	
340 345 350	
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Ser Ser Pro Gly Pro Lys Glu Ser His Tyr Ile Phe Lys Glu Phe Val	
355 360 365	
gaa ttg tta aag gat ttt taggggtttt taaaacagcg cttatagaga	1209
Glu Leu Leu Lys Asp Phe	
370 375	
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35 40 45	
Phe Val Val Phe Ser Met Pro Glu Ile Gly Val Val Gly Ala Asn Ser	
50 55 60	
Lys Asp Asp Glu Ser Phe Phe Ser Cys Ala Gly Val Leu Ala Arg His	
65 70 75 80	
Tyr Asn Glu Phe Phe Ser Asn Ser Arg Ala Asp Phe Ser Leu Ser Ala	
85 90 95	
Tyr Leu Lys Glu Arg Gly Val Leu Gly Val Cys Gly Val Asp Thr Arg	
100 105 110	
Ser Leu Ile Lys Thr Leu Arg His His Gly Cys Leu Met Met Val Ala	
115 120 125	
Ser Thr Ile Glu His Asp Lys Asn Lys Leu Glu Glu Ile Leu Lys Asn	
130 135 140	
Ala Pro Lys Ile Ser His Ser Pro Leu Val Ser Ser Val Ser Thr Pro	
145 150 155 160	

Lys Ile Thr Thr His Gln Arg Ala Thr Phe Asp Phe Lys Thr Leu Asp
 165 170 175
 Tyr Lys Pro Phe Asp Glu Lys Thr Ser His Lys Ile Ile Ala Val Leu
 180 185 190
 Asp Phe Gly Ala Lys Gly Asn Ile Leu Asn Glu Leu Gln Asn Val Gly
 195 200 205
 Leu Lys Ala Leu Ile Tyr Pro His His Thr Lys Ala Ser Glu Leu Ile
 210 215 220
 Lys Ala Tyr Glu Lys Lys Glu Ile Ser Gly Ile Phe Leu Ser Asn Gly
 225 230 235 240
 Pro Gly Asp Pro Leu Ser Leu Gln Gln Glu Ile Gly Glu Ile Lys Gln
 245 250 255
 Leu Ile Asn Ala Lys Ile Pro Met Leu Gly Ile Cys Leu Gly His Gln
 260 265 270
 Leu Leu Ser Ile Ala Gln Gly Tyr Pro Thr Tyr Lys Leu Lys Phe Gly
 275 280 285
 His His Gly Ser Asn His Pro Val Lys Asn Leu Lys Thr Asn Ala Val
 290 295 300
 Glu Ile Thr Ala Gln Asn His Asn Tyr Cys Val Pro Glu Asp Ile Glu
 305 310 315 320
 Glu Ile Ala Ile Ile Thr His Arg Asn Leu Phe Asp Asn Thr Ile Glu
 325 330 335
 Gly Val Arg Tyr Lys Asn Ala Pro Ile Ser Val Gln His His Pro
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 Val Glu Leu Leu Lys Asp Phe
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 gat att cgc aac gaa ttt tta caa ttt ttt caa aat aaa ggg cat gcc 166
 Asp Ile Arg Asn Glu Phe Leu Gln Phe Phe Gln Asn Lys Gly His Ala
 5 10 15
 gtt tat cct agc atg cct tta gtg cct aat gac gct acc ttg ctt ttt 214
 Val Tyr Pro Ser Met Pro Leu Val Pro Asn Asp Ala Thr Leu Leu Phe
 20 25 30
 acc aat gcc ggc atg gtg caa ttt aaa gat att ttt acc ggg att gtg 262
 Thr Asn Ala Gly Met Val Gln Phe Lys Asp Ile Phe Thr Gly Ile Val
 35 40 45
 cca cgc cct agc att cct aga gcg gca agc tcg caa ttg tgc atg cgc 310
 Pro Arg Pro Ser Ile Pro Arg Ala Ala Ser Ser Gln Leu Cys Met Arg
 50 55 60 65

gca ggc ggc aag cat aac gat ttg gaa aat gtc ggt tat acc gca agg Ala Gly Gly Lys His Asn Asp Leu Glu Asn Val Gly Tyr Thr Ala Arg 70 75 80	358
cac cac acg ctt ttt gaa atg cta ggg aat ttc tct ttt ggg gat tat His His Thr Leu Phe Glu Met Leu Gly Asn Phe Ser Phe Gly Asp Tyr 85 90 95	406
ttc aaa gaa gaa gcg atc ttg ttt gcg tgg gaa ttt gta acc aag aat Phe Lys Glu Glu Ala Ile Leu Phe Ala Trp Glu Phe Val Thr Lys Asn 100 105 110	454
tta ggg ttt aag cct aaa gat tta tac atc agc gtg cat gaa aag gac Leu Gly Phe Lys Pro Lys Asp Leu Tyr Ile Ser Val His Glu Lys Asp 115 120 125	502
gat gaa gcc gtt aaa tta tgg gaa aag ttt gtg cct gtt gat agg att Asp Glu Ala Val Lys Leu Trp Glu Lys Phe Val Pro Val Asp Arg Ile 130 135 140 145	550
aaa aaa atg ggc gat aaa gat aat ttt tgg caa atg ggc gat agc ggg Lys Lys Met Gly Asp Lys Asp Asn Phe Trp Gln Met Gly Asp Ser Gly 150 155 160	598
cct tgc ggg cct tgc agt gaa att tac att gat cag ggc gaa aaa cac Pro Cys Gly Pro Cys Ser Glu Ile Tyr Ile Asp Gln Gly Glu Lys His 165 170 175	646
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gaa att tgg aat ctg gtg ttc atg caa tac gaa cgc tct aat gat ggc Glu Ile Trp Asn Leu Val Phe Met Gln Tyr Glu Arg Ser Asn Asp Gly 195 200 205	742
gtt tta tcc ccc ttg cca aag cct agc att gat aca ggc atg gga tta Val Leu Ser Pro Leu Pro Lys Pro Ser Ile Asp Thr Gly Met Gly Leu 210 215 220 225	790
gaa agg gtg caa gcg cta tta gaa cat aag ctc aat aat ttt gat tct Glu Arg Val Gln Ala Leu Leu Glu His Lys Leu Asn Asn Phe Asp Ser 230 235 240	838
tca tta ttt gcg ccc cta atg gaa gaa atc agc gag ctt aca agc cta Ser Leu Phe Ala Pro Leu Met Glu Glu Ile Ser Glu Leu Thr Ser Leu 245 250 255	886
gat tat gcg agc gag ttc cag cca agc ttt agg gta gtg gcc gat cac Asp Tyr Ala Ser Glu Phe Gln Pro Ser Phe Arg Val Val Ala Asp His 260 265 270	934
gca aga gcg gta gca ttc ttg ctc gct caa ggg gtg cat ttc aat aag Ala Arg Ala Val Ala Phe Leu Leu Ala Gln Gly Val His Phe Asn Lys 275 280 285	982
gaa ggc cgt ggc tat gtt tta agg cgc att tta agg cga gcc tta agg Glu Gly Arg Gly Tyr Val Leu Arg Arg Ile Leu Arg Arg Ala Leu Arg	1030

Lys 530	Lys	Ala	Leu	Lys	Lys 535	Gly	Asp	Gln	Val	Ile 540	Ala	Gln	Val	Ser	Asp 545	
gag	cgc	ttt	gaa	atc	gcc	aaa	cac	cat	agt	gcg	act	cat	tta	ttg	cag	1798
Glu	Arg	Phe	Glu	Ile 550	Ala	Lys	His	His	Ser 555	Ala	Thr	His	Leu	Leu	Gln 560	
agc	gct	tta	aga	gaa	gtt	tta	ggc	tcg	cat	gtg	agt	caa	gcg	ggg	agt	1846
Ser	Ala	Leu	Arg	Glu 565	Val	Leu	Gly	Ser 570	His	Val	Ser	Gln	Ala	Gly	Ser 575	
tta	gtg	gaa	tcc	aag	cga	ttg	cgc	ttt	gat	ttc	tcg	cat	gct	aaa	gcg	1894
Leu	Val	Glu 580	Ser	Lys	Arg	Leu	Arg	Phe 585	Asp	Phe	Ser	His	Ala	Lys	Ala 590	
ctc	aat	gat	gaa	gag	cta	gaa	aaa	gta	gaa	gat	tta	gtc	aac	gct	caa	1942
Leu	Asn	Asp	Glu	Glu	Leu	Glu	Lys	Val	Glu	Asp	Leu	Val	Asn	Ala	Gln 605	
att	ttc	aag	cac	cta	aat	agc	cag	gtg	gag	cat	atg	cct	tta	aac	caa	1990
Ile	Phe	Lys	His	Leu	Asn 615	Ser	Gln	Val	Glu	His	Met	Pro	Leu	Asn	Gln 625	
gcc	aaa	gat	aag	gga	gcg	tta	gcg	tta	ttc	agt	gaa	aaa	tac	gct	gaa	2038
Ala	Lys	Asp	Lys	Gly 630	Ala	Leu	Ala	Leu	Phe	Ser	Glu	Lys	Tyr	Ala	Glu 640	
aat	gtg	cgg	gtg	gtg	agc	ttt	aaa	gaa	gcg	tcc	att	gaa	ttg	tgt	ggg	2086
Asn	Val	Arg	Val	Val	Ser	Phe	Lys	Glu 650	Ala	Ser	Ile	Glu	Leu	Cys	Gly 655	
ggc	att	cat	gtg	gaa	aat	act	ggg	ctt	att	ggg	ggg	ttt	agg	att	gta	2134
Gly	Ile	His	Val	Glu	Asn	Thr	Gly	Leu	Ile	Gly	Gly	Phe	Arg	Ile	Val 670	
aaa	gaa	agc	ggg	gtg	agt	agt	ggg	gtc	aga	cgc	att	gaa	gcg	gtg	tgc	2182
Lys	Glu	Ser	Gly	Val	Ser	Ser	Gly	Val	Arg	Arg	Ile	Glu	Ala	Val	Cys 685	
ggg	aaa	gcc	ttt	tac	caa	ctg	gct	aaa	gaa	gaa	aat	aaa	gag	ctt	aaa	2230
Gly	Lys	Ala	Phe	Tyr	Gln	Leu	Ala	Lys	Glu	Glu	Asn	Lys	Glu	Leu	Lys 705	
aac	gct	aag	act	tta	ttg	aaa	aat	aac	gat	gtg	atc	gcc	ggt	atc	aat	2278
Asn	Ala	Lys	Thr	Leu	Leu	Lys	Asn	Asn	Asp	Val	Ile	Ala	Gly	Ile	Asn 720	
aag	ctt	aaa	gag	agc	gtg	aaa	aac	agc	caa	aaa	gcc	ccc	gtt	tct	atg	2326
Lys	Leu	Lys	Glu	Ser	Val	Lys	Asn	Ser	Gln	Lys	Ala	Pro	Val	Ser	Met 735	
gat	tta	ccg	gtt	gaa	aaa	atc	cat	ggc	gtg	aat	ttg	gtg	gtg	ggc	gta	2374
Asp	Leu	Pro	Val	Glu	Lys	Ile	His	Gly	Val	Asn	Leu	Val	Val	Gly	Val 750	
gtg	gaa	caa	ggc	gac	att	aaa	gaa	atg	att	gac	cga	ttg	aaa	agt	aag	2422
Val	Glu	Gln	Gly	Asp	Ile	Lys	Glu	Met	Ile	Asp	Arg	Leu	Lys	Ser	Lys 765	

cat gaa aga ttg ctc gct atg gtg ttt aaa aaa gaa aat gag cga atc	2470
His Glu Arg Leu Leu Ala Met Val Phe Lys Lys Glu Asn Glu Arg Ile	
770 775 780 785	
act ctc gca tgc ggg gtg aaa aac gcg ccc ata aaa gcg aat gtg tgg	2518
Thr Leu Ala Cys Gly Val Lys Asn Ala Pro Ile Lys Ala Asn Val Trp	
790 795 800	
gct aat gaa gtg gcg caa att tta ggg ggc aaa ggg ggc ggg aga ggt	2566
Ala Asn Glu Val Ala Gln Ile Leu Gly Gly Lys Gly Gly Gly Arg Gly	
805 810 815	
gat ttt gcg agc gct gga ggc aag gat att gaa aat ttg caa gcc gca	2614
Asp Phe Ala Ser Ala Gly Gly Lys Asp Ile Glu Asn Leu Gln Ala Ala	
820 825 830	
ctc aat tta gcg aaa aat acc gct ctt aaa gct tta gag gga	2656
Leu Asn Leu Ala Lys Asn Thr Ala Leu Lys Ala Leu Glu Gly	
835 840 845	
tagcatggag cttatttttag gctctcaatc cagcactagg gcgaatctct taaaagagca	2716
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Phe Thr Asn Ala Gly Met Val Gln Phe Lys Asp Ile Phe Thr Gly Ile	
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Val Pro Arg Pro Ser Ile Pro Arg Ala Ala Ser Ser Gln Leu Cys Met	
50 55 60	
Arg Ala Gly Gly Lys His Asn Asp Leu Glu Asn Val Gly Tyr Thr Ala	
65 70 75 80	
Arg His His Thr Leu Phe Glu Met Leu Gly Asn Phe Ser Phe Gly Asp	
85 90 95	
Tyr Phe Lys Glu Glu Ala Ile Leu Phe Ala Trp Glu Phe Val Thr Lys	
100 105 110	
Asn Leu Gly Phe Lys Pro Lys Asp Leu Tyr Ile Ser Val His Glu Lys	
115 120 125	
Asp Asp Glu Ala Val Lys Leu Trp Glu Lys Phe Val Pro Val Asp Arg	
130 135 140	
Ile Lys Lys Met Gly Asp Lys Asp Asn Phe Trp Gln Met Gly Asp Ser	
145 150 155 160	
Gly Pro Cys Gly Pro Cys Ser Glu Ile Tyr Ile Asp Gln Gly Glu Lys	
165 170 175	
His Phe Lys Gly Ser Glu Asp Tyr Phe Gly Gly Glu Gly Asp Arg Phe	
180 185 190	
Leu Glu Ile Trp Asn Leu Val Phe Met Gln Tyr Glu Arg Ser Asn Asp	
195 200 205	
Gly Val Leu Ser Pro Leu Pro Lys Pro Ser Ile Asp Thr Gly Met Gly	
210 215 220	
Leu Glu Arg Val Gln Ala Leu Leu Glu His Lys Leu Asn Asn Phe Asp	

225					230				235				240			
Ser	Ser	Leu	Phe	Ala	Pro	Leu	Met	Glu	Glu	Ile	Ser	Glu	Leu	Thr	Ser	
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Leu	Asp	Tyr	Ala	Ser	Glu	Phe	Gln	Pro	Ser	Phe	Arg	Val	Val	Ala	Asp	
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His	Ala	Arg	Ala	Val	Ala	Phe	Leu	Leu	Ala	Gln	Gly	Val	His	Phe	Asn	
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Lys	Glu	Gly	Arg	Gly	Tyr	Val	Leu	Arg	Arg	Ile	Leu	Arg	Arg	Ala	Leu	
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Arg	His	Gly	Tyr	Leu	Met	Gly	Leu	Lys	Glu	Ala	Phe	Leu	Tyr	Lys	Val	
305					310					315					320	
Val	Gly	Val	Val	Cys	Glu	Gln	Phe	Ala	Asn	Thr	His	Ala	Tyr	Leu	Lys	
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Glu	Ser	Lys	Glu	Met	Val	Val	Lys	Glu	Cys	Phe	Glu	Glu	Glu	Glu	His	
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Phe	Leu	Glu	Thr	Leu	Glu	Ser	Gly	Met	Glu	Leu	Phe	Asn	Leu	Ser	Leu	
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Lys	His	Leu	Asn	Glu	Asn	Lys	Ile	Phe	Asp	Gly	Lys	Ile	Ala	Phe	Lys	
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Leu	Tyr	Asp	Thr	Phe	Gly	Phe	Pro	Leu	Asp	Leu	Thr	Asn	Asp	Met	Leu	
385					390					395					400	
Arg	Ser	His	Gly	Ala	Cys	Ala	Asp	Met	Gln	Gly	Phe	Glu	Leu	Cys	Met	
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Gln	Glu	Gln	Val	Lys	Arg	Ser	Lys	Ala	Ser	Trp	Lys	Gly	Lys	Gln	Asn	
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Asn	Ala	Asp	Phe	Ser	Ala	Ile	Leu	Asn	Ala	Tyr	Ala	Pro	Asn	Val	Phe	
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Val	Gly	Tyr	Glu	Thr	Thr	Glu	Cys	Ser	Ala	Lys	Val	Leu	Gly	Phe	Phe	
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Asp	Ser	Asp	Phe	Lys	Glu	Ile	Thr	Asp	Ala	Asn	Pro	Asn	Gln	Glu	Val	
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Trp	Val	Leu	Leu	Glu	Lys	Thr	Pro	Phe	Tyr	Ala	Glu	Gly	Gly	Gly	Ala	
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Ile	Gly	Asp	Arg	Gly	Ala	Leu	Phe	Lys	Asp	Asn	Gly	Glu	Val	Ala	Ile	
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Val	Leu	Asp	Thr	Lys	Asn	Phe	Phe	Gly	Leu	Asn	Phe	Ser	Leu	Leu	Glu	
		515					520					525				
Ile	Lys	Lys	Ala	Leu	Lys	Lys	Gly	Asp	Gln	Val	Ile	Ala	Gln	Val	Ser	
	530					535					540					
Asp	Glu	Arg	Phe	Glu	Ile	Ala	Lys	His	His	Ser	Ala	Thr	His	Leu	Leu	
545					550					555					560	
Gln	Ser	Ala	Leu	Arg	Glu	Val	Leu	Gly	Ser	His	Val	Ser	Gln	Ala	Gly	
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Ser	Leu	Val	Glu	Ser	Lys	Arg	Leu	Arg	Phe	Asp	Phe	Ser	His	Ala	Lys	
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Lys Asn Ala Lys Thr Leu Leu Lys Asn Asn Asp Val Ile Ala Gly Ile
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Asn Lys Leu Lys Glu Ser Val Lys Asn Ser Gln Lys Ala Pro Val Ser
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Met Asp Leu Pro Val Glu Lys Ile His Gly Val Asn Leu Val Val Gly
          740          745          750
Val Val Glu Gln Gly Asp Ile Lys Glu Met Ile Asp Arg Leu Lys Ser
          755          760          765
Lys His Glu Arg Leu Leu Ala Met Val Phe Lys Lys Glu Asn Glu Arg
          770          775          780
Ile Thr Leu Ala Cys Gly Val Lys Asn Ala Pro Ile Lys Ala Asn Val
785          790          795          800
Trp Ala Asn Glu Val Ala Gln Ile Leu Gly Gly Lys Gly Gly Gly Arg
          805          810          815
Gly Asp Phe Ala Ser Ala Gly Gly Lys Asp Ile Glu Asn Leu Gln Ala
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Ala Leu Asn Leu Ala Lys Asn Thr Ala Leu Lys Ala Leu Glu Gly
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                               Met Phe Asn Lys Val
                               1          5

att atg gta ggg cgt ttg acc agg aat gtg gag ttg aaa tat ttg cct      162
Ile Met Val Gly Arg Leu Thr Arg Asn Val Glu Leu Lys Tyr Leu Pro
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agc ggt tcg gct gcg gct aca ata ggt tta gcc aca agc agg cgt ttt      210
Ser Gly Ser Ala Ala Ala Thr Ile Gly Leu Ala Thr Ser Arg Arg Phe
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aaa aaa caa gac ggc acg cta ggc gaa gag gtg tgc ttt ata gat gcg      258
Lys Lys Gln Asp Gly Thr Leu Gly Glu Glu Val Cys Phe Ile Asp Ala
                               40          45          50

cgt ttg ttt ggg cga acg gct gaa atc gct aac cag tat ttg agc aag      306
Arg Leu Phe Gly Arg Thr Ala Glu Ile Ala Asn Gln Tyr Leu Ser Lys
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ggt tca agc gtt ttg ata gaa ggg cgt ttg act tat gag agt tgg atg      354
Gly Ser Ser Val Leu Ile Glu Gly Arg Leu Thr Tyr Glu Ser Trp Met
                               70          75          80          85

gat caa acg ggc aaa aaa aat tcc cgc cac act atc aca gcg gac tcg      402
Asp Gln Thr Gly Lys Lys Asn Ser Arg His Thr Ile Thr Ala Asp Ser
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ttg caa ttt atg gat aaa aag tca gac aat ccc caa gca aac gct atg      450

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Leu	Gln	Phe	Met	Asp	Lys	Lys	Ser	Asp	Asn	Pro	Gln	Ala	Asn	Ala	Met		
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Gln	Asp	Ser	Ile	Met	His	Glu	Asn	Ser	Asn	Asn	Ala	Tyr	Pro	Ala	Asn		
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cat	aac	gct	ccc	agc	caa	gat	cct	ttt	aac	caa	gct	tat	gcg	caa	aac	546	
His	Asn	Ala	Pro	Ser	Gln	Asp	Pro	Phe	Asn	Gln	Ala	Tyr	Ala	Gln	Asn		
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Ala	Tyr	Ala	Lys	Glu	Asn	Leu	Gln	Ala	Gln	Pro	Ser	Lys	Tyr	Gln	Asn		
					155					160					165		
agc	gtg	cct	gaa	atc	aat	att	gat	gaa	gaa	gaa	atc	ccc	ttt			636	
Ser	Val	Pro	Glu	Ile	Asn	Ile	Asp	Glu	Glu	Glu	Ile	Pro	Phe				
				170					175								
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 <211> 179
 <212> PRT
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Thr	Ser	Arg	Arg	Phe	Lys	Lys	Gln	Asp	Gly	Thr	Leu	Gly	Glu	Glu	Val		
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Cys	Phe	Ile	Asp	Ala	Arg	Leu	Phe	Gly	Arg	Thr	Ala	Glu	Ile	Ala	Asn		
	50				55					60							
Gln	Tyr	Leu	Ser	Lys	Gly	Ser	Ser	Val	Leu	Ile	Glu	Gly	Arg	Leu	Thr		
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Tyr	Glu	Ser	Trp	Met	Asp	Gln	Thr	Gly	Lys	Lys	Asn	Ser	Arg	His	Thr		
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Ile	Thr	Ala	Asp	Ser	Leu	Gln	Phe	Met	Asp	Lys	Lys	Ser	Asp	Asn	Pro		
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Gln	Ala	Asn	Ala	Met	Gln	Asp	Ser	Ile	Met	His	Glu	Asn	Ser	Asn	Asn		
		115				120						125					
Ala	Tyr	Pro	Ala	Asn	His	Asn	Ala	Pro	Ser	Gln	Asp	Pro	Phe	Asn	Gln		
	130					135					140						
Ala	Tyr	Ala	Gln	Asn	Ala	Tyr	Ala	Lys	Glu	Asn	Leu	Gln	Ala	Gln	Pro		
145				150					155						160		
Ser	Lys	Tyr	Gln	Asn	Ser	Val	Pro	Glu	Ile	Asn	Ile	Asp	Glu	Glu	Glu		
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Ile	Pro	Phe															

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<220>

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<400> 167

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aactttttaaa aaaggctgaa tgaaagaata atg aaa tta aaa tct ttt ggg gtt	114
Met Lys Leu Lys Ser Phe Gly Val	
1 5	
ttt gga aat ccc att aag cat tcc aaa tcg ccc tta atc cat aac gct	162
Phe Gly Asn Pro Ile Lys His Ser Lys Ser Pro Leu Ile His Asn Ala	
10 15 20	
tgt ttt tta act ttt caa aaa gaa tta agg ttt ttg ggg cat tac cac	210
Cys Phe Leu Thr Phe Gln Lys Glu Leu Arg Phe Leu Gly His Tyr His	
25 30 35 40	
ccc ata tta ctc cct tta gaa agc cac atc aaa agc gag ttt ttg cat	258
Pro Ile Leu Leu Pro Leu Glu Ser His Ile Lys Ser Glu Phe Leu His	
45 50 55	
ttg gga ttg agt ggg gct aat gta acc tta ccc ttt aaa gaa agg gcg	306
Leu Gly Leu Ser Gly Ala Asn Val Thr Leu Pro Phe Lys Glu Arg Ala	
60 65 70	
ttt caa gtt tgc gat aaa atc aaa ggt atc gcg ctt gaa tgc gga gcg	354
Phe Gln Val Cys Asp Lys Ile Lys Gly Ile Ala Leu Glu Cys Gly Ala	
75 80 85	
gtc aat acg ctt gtt tta gaa aat gat gag ctt gtg ggt tac aat acc	402
Val Asn Thr Leu Val Leu Glu Asn Asp Glu Leu Val Gly Tyr Asn Thr	
90 95 100	
gac gct tta ggg ttt tat ctt tct tta aag caa aaa aac tat caa aac	450
Asp Ala Leu Gly Phe Tyr Leu Ser Leu Lys Gln Lys Asn Tyr Gln Asn	
105 110 115 120	
gct ttg att tta gga gct ggg ggg agc gct aaa gcc cta gcg tgt gaa	498
Ala Leu Ile Leu Gly Ala Gly Gly Ser Ala Lys Ala Leu Ala Cys Glu	
125 130 135	
ttg aaa aaa caa ggc tta caa gtg agc gtg ttg aac cgc tct tct agg	546
Leu Lys Lys Gln Gly Leu Gln Val Ser Val Leu Asn Arg Ser Ser Arg	
140 145 150	
gga ttg gat ttt ttc caa cgc ctg ggc tgt gat tgt ttt atg gag cct	594
Gly Leu Asp Phe Phe Gln Arg Leu Gly Cys Asp Cys Phe Met Glu Pro	
155 160 165	
cct aaa agc gct ttt gat ttg att att aac gcc act tca gcg agt ttg	642
Pro Lys Ser Ala Phe Asp Leu Ile Ile Asn Ala Thr Ser Ala Ser Leu	
170 175 180	
cat aac gaa ttg cct ttg aat aaa gag gtt ttg aaa ggg tat ttt aaa	690
His Asn Glu Leu Pro Leu Asn Lys Glu Val Leu Lys Gly Tyr Phe Lys	
185 190 195 200	
gag ggc aag ctc gct tat gat ttg gcg tat ggg ttt tta acg ccc ttt	738
Glu Gly Lys Leu Ala Tyr Asp Leu Ala Tyr Gly Phe Leu Thr Pro Phe	

205

210

215

ttg tct tta gcc aaa gag tta aaa acc cct ttt caa gac gga aaa gac 786
 Leu Ser Leu Ala Lys Glu Leu Lys Thr Pro Phe Gln Asp Gly Lys Asp
 220 225 230

atg ctc atc tat caa gct gct tta agt ttt gaa aaa ttc agc gct tct 834
 Met Leu Ile Tyr Gln Ala Ala Leu Ser Phe Glu Lys Phe Ser Ala Ser
 235 240 245

caa atc cct tat tca aaa gcg ttt gaa gtc atg cga agt gtt ttt 879
 Gln Ile Pro Tyr Ser Lys Ala Phe Glu Val Met Arg Ser Val Phe
 250 255 260

tgatgcaagg gtttttaaga agcctgtttt ttgggggttaa aaagatccct aaaccattcg 939
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<211> 263

<212> PRT

<213> Helicobacter pylori

<400> 168

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 20 25 30
 Leu Arg Phe Leu Gly His Tyr His Pro Ile Leu Leu Pro Leu Glu Ser
 35 40 45
 His Ile Lys Ser Glu Phe Leu His Leu Gly Leu Ser Gly Ala Asn Val
 50 55 60
 Thr Leu Pro Phe Lys Glu Arg Ala Phe Gln Val Cys Asp Lys Ile Lys
 65 70 75 80
 Gly Ile Ala Leu Glu Cys Gly Ala Val Asn Thr Leu Val Leu Glu Asn
 85 90 95
 Asp Glu Leu Val Gly Tyr Asn Thr Asp Ala Leu Gly Phe Tyr Leu Ser
 100 105 110
 Leu Lys Gln Lys Asn Tyr Gln Asn Ala Leu Ile Leu Gly Ala Gly Gly
 115 120 125
 Ser Ala Lys Ala Leu Ala Cys Glu Leu Lys Lys Gln Gly Leu Gln Val
 130 135 140
 Ser Val Leu Asn Arg Ser Ser Arg Gly Leu Asp Phe Phe Gln Arg Leu
 145 150 155 160
 Gly Cys Asp Cys Phe Met Glu Pro Pro Lys Ser Ala Phe Asp Leu Ile
 165 170 175
 Ile Asn Ala Thr Ser Ala Ser Leu His Asn Glu Leu Pro Leu Asn Lys
 180 185 190
 Glu Val Leu Lys Gly Tyr Phe Lys Glu Gly Lys Leu Ala Tyr Asp Leu
 195 200 205
 Ala Tyr Gly Phe Leu Thr Pro Phe Leu Ser Leu Ala Lys Glu Leu Lys
 210 215 220
 Thr Pro Phe Gln Asp Gly Lys Asp Met Leu Ile Tyr Gln Ala Ala Leu
 225 230 235 240
 Ser Phe Glu Lys Phe Ser Ala Ser Gln Ile Pro Tyr Ser Lys Ala Phe
 245 250 255
 Glu Val Met Arg Ser Val Phe
 260

<210> 169

0909013 060901

<211> 1080
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<220>
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 <222> (47)...(1033)

<400> 169

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tat atc att gaa acc ctg att aaa att ttg att tta gtc gct gtt ttt      103
Tyr Ile Ile Glu Thr Leu Ile Lys Ile Leu Ile Leu Val Ala Val Phe
   5                               10                               15

tcg gct tta gga ggc ttt gcc act tat att gaa agg aaa gtg tta gcc      151
Ser Ala Leu Gly Gly Phe Ala Thr Tyr Ile Glu Arg Lys Val Leu Ala
  20                               25                               30                               35

tat ttc caa cgc cgt tta ggg cct tgt tat gtg ggg cct ttt ggg ctt      199
Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro Phe Gly Leu
                               40                               45                               50

ttg caa gtc gca gca gac ggc att aag ctt ttc act aaa gaa gac att      247
Leu Gln Val Ala Ala Asp Gly Ile Lys Leu Phe Thr Lys Glu Asp Ile
                               55                               60                               65

atc cct caa ggc gcg aac aaa ttc att ttc acg cta gcg ccc att att      295
Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala Pro Ile Ile
   70                               75                               80

gcg atg gtg agt gcg ttt gtg tcc atg gcg cct atc ccc ttt ttc cct      343
Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro Phe Phe Pro
   85                               90                               95

aat ttc act ctg ttt ggc tat gag atc aag ccc ctt att tct gac atc      391
Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile Ser Asp Ile
  100                               105                               110                               115

aac att ggc ttt ttg ttt ttc tta gcc gtg ggt tcg gca ggg att tat      439
Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala Gly Ile Tyr
                               120                               125                               130

gcg cct att tta gcc ggg ctt gcc tct aat aac aaa tac tct tta att      487
Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser Leu Ile
                               135                               140                               145

ggc tcc gca aga gcg acg atc caa ctg ctc agc ttt gaa gtg gtc agc      535
Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val Val Ser
  150                               155                               160

act tta acc att cta gcc ccc tta atg gtg gta gga tcg ctc tct tta      583
Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu Ser Leu
  165                               170                               175

gtg gaa atc aat cat tac caa agc ggt ggg ttt tta gac tgg ctt gtg      631
Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp Leu Val

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180	185	190	195	
ttt aag cag cct cta gcg ttt gtt ttg ttt ttg atc gca agt tat gcc				679
Phe Lys Gln Pro	Leu Ala Phe Val	Leu Phe Leu Ile	Ala Ser Tyr Ala	
	200	205	210	
gaa ttg aat cga acc ccc ttt gac ttg cta gag cat gaa gcc gag atc				727
Glu Leu Asn Arg Thr	Pro Phe Asp	Leu Leu Glu His	Glu Ala Glu Ile	
	215	220	225	
gtg gcg ggg tat tgc acc gaa tac agc ggc ttg aaa tgg ggc atg ttc				775
Val Ala Gly Tyr Cys Thr	Glu Tyr Ser	Gly Leu Lys Trp	Gly Met Phe	
	230	235	240	
ttt tta gcg gaa tac gcg cat tta ttc gct ttt tct ttt gtg att tct				823
Phe Leu Ala Glu Tyr	Ala His Leu Phe	Ala Phe Ser	Phe Val Ile Ser	
	245	250	255	
att gtg ttt ttt ggc ggg ttt aac gca tgg ggc ttt atc cct gga ggc				871
Ile Val Phe Phe Gly Gly	Phe Asn Ala Trp	Gly Phe Ile	Pro Gly Gly	
	260	265	270	275
ata gcg att ttg att aaa gcg ggc ttt ttt gtc ttt tta tcc atg tgg				919
Ile Ala Ile Leu Ile Lys	Ala Gly Phe Phe	Val Phe Leu	Ser Met Trp	
	280	285	290	
gtt aga gcg act tat ccg cat gtg cgc cca gac caa ctg atg gat atg				967
Val Arg Ala Thr Tyr	Pro His Val Arg	Pro Asp Gln	Leu Met Asp Met	
	295	300	305	
tgc tgg aaa atc atg ctg cct tta gcg tta ttg aac att gtg cta acg				1015
Cys Trp Lys Ile Met Leu	Pro Leu Ala Leu	Leu Asn Ile	Val Leu Thr	
	310	315	320	
ggc att atc att tta att taaaggaggt tttatggcca aacaagaata				1063
Gly Ile Ile Ile Leu Ile				
	325			
caagcaactt cctaaac				1080
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20 25 30				
Val Leu Ala Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro				
35 40 45				
Phe Gly Leu Leu Gln Val Ala Ala Asp Gly Ile Lys Leu Phe Thr Lys				
50 55 60				
Glu Asp Ile Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala				
65 70 75 80				
Pro Ile Ile Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro				
85 90 95				
Phe Phe Pro Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile				

100 105 110
 Ser Asp Ile Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala
 115 120 125
 Gly Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr
 130 135 140
 Ser Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu
 145 150 155 160
 Val Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser
 165 170 175
 Leu Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp
 180 185 190
 Trp Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala
 195 200 205
 Ser Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu
 210 215 220
 Ala Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp
 225 230 235 240
 Gly Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe
 245 250 255
 Val Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile
 260 265 270
 Pro Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu
 275 280 285
 Ser Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu
 290 295 300
 Met Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile
 305 310 315 320
 Val Leu Thr Gly Ile Ile Ile Leu Ile
 325

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<220>
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 Met Asn Lys
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 Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu
 5 10 15

 gtg cct gca tta aga gaa tta gaa cag gcg ttt gat gcg tgt ttg aaa 152
 Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys
 20 25 30 35

 gat gaa aaa ttc caa aaa gaa tat ttt cgt ctt tta aag gat ttt gtg 200
 Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys Asp Phe Val
 40 45 50

 ggc cgt cct agc cct tta acc ttg tgt caa aat atc gtt tct aac cct 248
 Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val Ser Asn Pro
 55 60 65

090601Z JUL 71

[illegible]

195	200	205
Glu Val Lys Ser Gln Ile	Leu Glu Lys Glu Asn Arg	Leu Pro Asp Tyr
210	215	220
Val Ile Ala Cys Val Gly	Gly Ser Asn Ala Ile	Gly Ile Phe Ser
225	230	235
Ala Phe Leu Asn Asp Lys	Glu Val Lys Leu Ile	Gly Val Glu Pro Ala
245	250	255
Gly Leu Gly Leu Glu Thr	Asn Lys His Gly Ala Thr	Leu Asn Lys Gly
260	265	270
Arg Val Gly Ile Leu His	Gly Asn Lys Thr Tyr Leu	Leu Gln Asp Asp
275	280	285
Glu Gly Gln Ile Ala Glu	Ser His Ser Ile Ser Ala	Gly Leu Asp Tyr
290	295	300
Pro Gly Val Gly Pro Glu	Ser His Ser Tyr Leu Lys	Glu Ser Gly Arg Ala
305	310	315
Val Tyr Glu Ser Ala Ser	Asp Ala Glu Ala Leu Glu	Ala Phe Lys Leu
325	330	335
Leu Cys Gln Lys Glu Gly	Ile Ile Pro Ala Leu Glu	Ser Ser His Ala
340	345	350
Leu Ala Tyr Ala Leu Lys	Leu Ala Gln Lys Cys Glu	Glu Glu Ser Ile
355	360	365
Ile Val Val Asn Leu Ser	Gly Arg Gly Asp Lys Asp	Leu Ser Thr Val
370	375	380
Tyr Asn Ala Leu Lys Gly	Gly Leu Lys	
385	390	

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 <211> 559
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (31)...(513)

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1 5	
gat tgg gaa tat caa tgg gca gtg gct cta gtc tat acg ata tgt atc	102
Asp Trp Glu Tyr Gln Trp Ala Val Ala Leu Val Tyr Thr Ile Cys Ile	
10 15 20	
tcc ata aac gct agg att ttt tat gac ata gat ggt tca gct agc gat	150
Ser Ile Asn Ala Arg Ile Phe Tyr Asp Ile Asp Gly Ser Ala Ser Asp	
25 30 35 40	
tcg att ttt gac cct aaa aat agc tat tat atg tgg cta gtg ggt cta	198
Ser Ile Phe Asp Pro Lys Asn Ser Tyr Tyr Met Trp Leu Val Gly Leu	
45 50 55	
ata gcg gct ttg ttg tct aac ctt tta ttt gac cca cga ggt agg gat	246
Ile Ala Ala Leu Leu Ser Asn Leu Leu Phe Asp Pro Arg Gly Arg Asp	
60 65 70	
tgt tat aaa tct ttc caa gta aga tac cct agg ttt ctc aaa gcc att	294
Cys Tyr Lys Ser Phe Gln Val Arg Tyr Pro Arg Phe Leu Lys Ala Ile	
75 80 85	

ttt aag gct agg ttt ttt ggc gcg ttt tat aac gct gtg tta gga tca 342
Phe Lys Ala Arg Phe Phe Gly Ala Phe Tyr Asn Ala Val Leu Gly Ser
90 95 100

agg cta agg gat ttt tat gtg atg ctt tta acg ata ccc ttt att gcc 390
Arg Leu Arg Asp Phe Tyr Val Met Leu Leu Thr Ile Pro Phe Ile Ala
105 110 115 120

gct atc cat gag gtt tcg gcg tat tac ggg cat cct agc aac ttc ctt 438
Ala Ile His Glu Val Ser Ala Tyr Tyr Gly His Pro Ser Asn Phe Leu
125 130 135

ata gag ggt ttg gtc att ctt ggc ctt gtg tgt gtt ttt ggg att tgt 486
Ile Glu Gly Leu Val Ile Leu Gly Leu Val Cys Val Phe Gly Ile Cys
140 145 150

tct agg ctt tgc gct aaa tta ggg tgg tgatttaact caaatagcat 533
Ser Arg Leu Cys Ala Lys Leu Gly Trp
155 160

taaatggagg ggggagtaaa aaatta 559

<210> 174
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<212> PRT
<213> Helicobacter pylori

<400> 174
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Ala Leu Val Tyr Thr Ile Cys Ile Ser Ile Asn Ala Arg Ile Phe Tyr
20 25 30
Asp Ile Asp Gly Ser Ala Ser Asp Ser Ile Phe Asp Pro Lys Asn Ser
35 40 45
Tyr Tyr Met Trp Leu Val Gly Leu Ile Ala Ala Leu Leu Ser Asn Leu
50 55 60
Leu Phe Asp Pro Arg Gly Arg Asp Cys Tyr Lys Ser Phe Gln Val Arg
65 70 75 80
Tyr Pro Arg Phe Leu Lys Ala Ile Phe Lys Ala Arg Phe Phe Gly Ala
85 90 95
Phe Tyr Asn Ala Val Leu Gly Ser Arg Leu Arg Asp Phe Tyr Val Met
100 105 110
Leu Leu Thr Ile Pro Phe Ile Ala Ala Ile His Glu Val Ser Ala Tyr
115 120 125
Tyr Gly His Pro Ser Asn Phe Leu Ile Glu Gly Leu Val Ile Leu Gly
130 135 140
Leu Val Cys Val Phe Gly Ile Cys Ser Arg Leu Cys Ala Lys Leu Gly
145 150 155 160
Trp

<210> 175
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<213> Helicobacter pylori

<220>
<221> CDS

095591.062901

098571-0601

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							Met	Leu									
							1										
ata	acc	acc	caa	cta	tcc	aaa	cga	ttt	tac	gcc	aca	ctc	gct	ctt	tct		106
Ile	Thr	Thr	Gln	Leu	Ser	Lys	Arg	Phe	Tyr	Ala	Thr	Leu	Ala	Leu	Ser		
		5					10					15					
tgc	gtg	ttt	tta	acc	atc	act	aac	att	ctt	gtc	aaa	ggc	tcg	ttt	atc		154
Cys	Val	Phe	Leu	Thr	Ile	Thr	Asn	Ile	Leu	Val	Lys	Gly	Ser	Phe	Ile		
	20					25					30						
aat	ctt	tta	gca	ggg	ctt	agt	ggg	gtt	ttg	tat	gcg	ttt	ttt	gcc	gga		202
Asn	Leu	Leu	Ala	Gly	Leu	Ser	Gly	Val	Leu	Tyr	Ala	Phe	Phe	Ala	Gly		
	35				40					45					50		
gaa	agg	caa	acg	att	tgc	ttt	gtg	ttt	ggg	ctt	gtt	tat	aat	ttg	agt		250
Glu	Arg	Gln	Thr	Ile	Cys	Phe	Val	Phe	Gly	Leu	Val	Tyr	Asn	Leu	Ser		
				55					60					65			
tac	gct	tat	gtc	gct	tat	cag	tgg	aaa	tta	aac	gct	gat	gtg	att	tta		298
Tyr	Ala	Tyr	Val	Ala	Tyr	Gln	Trp	Lys	Leu	Asn	Ala	Asp	Val	Ile	Leu		
			70					75					80				
tgc	ctt	ttt	ttg	tat	atg	cca	gta	acg	att	tat	ggg	ctg	ttc	gca	tgg		346
Cys	Leu	Phe	Leu	Tyr	Met	Pro	Val	Thr	Ile	Tyr	Gly	Leu	Phe	Ala	Trp		
		85					90					95					
aaa	aag	aca	gag	cag	cat	gaa	ggc	gtt	atc	aag	gct	caa	aaa	ctt	tcc		394
Lys	Lys	Thr	Glu	Gln	His	Glu	Gly	Val	Ile	Lys	Ala	Gln	Lys	Leu	Ser		
	100					105					110						
aaa	aat	tgg	cgt	ttt	ata	ctc	att	tta	ggc	gta	ggg	gtt	tta	act	tgt		442
Lys	Asn	Trp	Arg	Phe	Ile	Leu	Ile	Leu	Gly	Val	Gly	Val	Leu	Thr	Cys		
	115				120					125					130		
gtg	agc	gct	ttg	ttt	ttt	aaa	gag	att	aaa	acg	aat	ttt	tta	tgg	gca		490
Val	Ser	Ala	Leu	Phe	Phe	Lys	Glu	Ile	Lys	Thr	Asn	Phe	Leu	Trp	Ala		
				135					140					145			
gag	agt	ttt	aat	ttc	gtc	atc	ttt	att	att	gct	ttt	att	tta	cag	gtt		538
Glu	Ser	Phe	Asn	Phe	Val	Ile	Phe	Ile	Ile	Ala	Phe	Ile	Leu	Gln	Val		
			150					155					160				
ttg	cgc	tat	ata	gaa	aat	tat	gcg	cta	gta	act	ttg	ggg	aat	atc	gta		586
Leu	Arg	Tyr	Ile	Glu	Asn	Tyr	Ala	Leu	Val	Thr	Leu	Gly	Asn	Ile	Val		
		165					170					175					
tcc	att	atc	gtg	tgg	ttt	tgt	att	ttt	caa	att	tct	aca	gag	agc	ttg		634
Ser	Ile	Ile	Val	Trp	Phe	Cys	Ile	Phe	Gln	Ile	Ser	Thr	Glu	Ser	Leu		
			180			185					190						

gcg tta tta aag aat tta gcg atc gct ttg att gag cat aac aaa att 152
Ala Leu Leu Lys Asn Leu Ala Ile Ala Leu Ile Glu His Asn Lys Ile
20 25 30

gaa aca ggg att tat aag gct aag gaa ttg cgc agt tac att gag aaa 200
Glu Thr Gly Ile Tyr Lys Ala Lys Glu Leu Arg Ser Tyr Ile Glu Lys
35 40 45 50

ttg acg aca gcg gct cgt gtg ggc gat ttt aat gcg cac cgc cat gtt 248
Leu Thr Thr Ala Ala Arg Val Gly Asp Phe Asn Ala His Arg His Val
55 60 65

ttt gca tat ttg caa aac aaa gaa gcc acc cac aag ctt gta act gaa 296
Phe Ala Tyr Leu Gln Asn Lys Glu Ala Thr His Lys Leu Val Thr Glu
70 75 80

atc gcg ccc aaa tac gcg caa agg aat ggc gga tac acc agg atc caa 344
Ile Ala Pro Lys Tyr Ala Gln Arg Asn Gly Gly Tyr Thr Arg Ile Gln
85 90 95

cgc acc act ttt aga aga ggg gac gct tcc act cta gcc acc att gaa 392
Arg Thr Thr Phe Arg Arg Gly Asp Ala Ser Thr Leu Ala Thr Ile Glu
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Phe Val
115

gct 451

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<212> PRT
<213> Helicobacter pylori

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Arg Lys Ala Leu Lys Asn Leu Ala Ile Ala Leu Ile Glu His Asn
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Lys Ile Glu Thr Gly Ile Tyr Lys Ala Lys Glu Leu Arg Ser Tyr Ile
35 40 45
Glu Lys Leu Thr Thr Ala Ala Arg Val Gly Asp Phe Asn Ala His Arg
50 55 60
His Val Phe Ala Tyr Leu Gln Asn Lys Glu Ala Thr His Lys Leu Val
65 70 75 80
Thr Glu Ile Ala Pro Lys Tyr Ala Gln Arg Asn Gly Gly Tyr Thr Arg
85 90 95
Ile Gln Arg Thr Thr Phe Arg Arg Gly Asp Ala Ser Thr Leu Ala Thr
100 105 110
Ile Glu Phe Val
115

<210> 179
<211> 1204
<212> DNA
<213> Helicobacter pylori

<220>
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 <222> (36)...(1142)

<400> 179

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	Val Glu Leu Ser Tyr Tyr	
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gaa att tta gaa gtg gaa aaa cac agc aac caa gag acc att aaa aag	101	
Glu Ile Leu Glu Val Glu Lys His Ser Asn Gln Glu Thr Ile Lys Lys		
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tct tac aga aag ctg gct tta aaa tac cac cca gac aga aac gcc ggc	149	
Ser Tyr Arg Lys Leu Ala Leu Lys Tyr His Pro Asp Arg Asn Ala Gly		
	25 30 35	
gat aaa gaa gcc gaa gaa aaa ttc aag ctc atc aat gaa gcc tat ggg	197	
Asp Lys Glu Ala Glu Glu Lys Phe Lys Leu Ile Asn Glu Ala Tyr Gly		
	40 45 50	
gtg tta agc gat gaa aag aag cgg gcc tta tac gac agg tat ggt aaa	245	
Val Leu Ser Asp Glu Lys Lys Arg Ala Leu Tyr Asp Arg Tyr Gly Lys		
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Lys Gly Leu Asn Gln Ala Gly Ala Ser Gln Gly Asp Phe Ser Asp Phe		
	75 80 85	
ttt gaa gat tta ggc tcg ttt ttt gaa gac gct ttt ggg ttt ggc gct	341	
Phe Glu Asp Leu Gly Ser Phe Phe Glu Asp Ala Phe Gly Phe Gly Ala		
	90 95 100	
agg ggg agt aaa agg caa aaa agc tct atc gca ccg gat tat ttg caa	389	
Arg Gly Ser Lys Arg Gln Lys Ser Ser Ile Ala Pro Asp Tyr Leu Gln		
	105 110 115	
acc ctt gaa ttg agt ttc aaa gaa gcg gtt ttt ggc tgt aaa aaa acc	437	
Thr Leu Glu Leu Ser Phe Lys Glu Ala Val Phe Gly Cys Lys Lys Thr		
	120 125 130	
att aaa gtc caa tac cag agc gtt tgt gaa agt tgc gat ggc acg ggc	485	
Ile Lys Val Gln Tyr Gln Ser Val Cys Glu Ser Cys Asp Gly Thr Gly		
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gct aaa gac aaa gcc cta gag act tgc aag caa tgc aat ggg cag ggc	533	
Ala Lys Asp Lys Ala Leu Glu Thr Cys Lys Gln Cys Asn Gly Gln Gly		
	155 160 165	
cag gtg ttt atg cgt caa ggt ttt atg agt ttt gcg caa act tgt ggc	581	
Gln Val Phe Met Arg Gln Gly Phe Met Ser Phe Ala Gln Thr Cys Gly		
	170 175 180	
gcg tgt caa ggc aag ggc aag atc gtt aaa acc cca tgc caa gcg tgc	629	
Ala Cys Gln Gly Lys Gly Lys Ile Val Lys Thr Pro Cys Gln Ala Cys		
	185 190 195	
aag ggt aaa acc tat atc ctt aaa gat gaa gaa att gat gcg ata atc	677	
Lys Gly Lys Thr Tyr Ile Leu Lys Asp Glu Glu Ile Asp Ala Ile Ile		

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Gly Asp Phe Ser Asp Phe Phe Glu Asp Leu Gly Ser Phe Phe Glu Asp						
	85			90		95
Ala Phe Gly Phe Gly Ala Arg Gly Ser Lys Arg Gln Lys Ser Ser Ile						
	100			105		110
Ala Pro Asp Tyr Leu Gln Thr Leu Glu Leu Ser Phe Lys Glu Ala Val						
	115			120		125
Phe Gly Cys Lys Lys Thr Ile Lys Val Gln Tyr Gln Ser Val Cys Glu						
	130			135		140
Ser Cys Asp Gly Thr Gly Ala Lys Asp Lys Ala Leu Glu Thr Cys Lys						
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Gln Cys Asn Gly Gln Gly Gln Val Phe Met Arg Gln Gly Phe Met Ser						
	165			170		175
Phe Ala Gln Thr Cys Gly Ala Cys Gln Gly Lys Gly Lys Ile Val Lys						
	180			185		190
Thr Pro Cys Gln Ala Cys Lys Gly Lys Thr Tyr Ile Leu Lys Asp Glu						
	195			200		205
Glu Ile Asp Ala Ile Ile Pro Glu Gly Ile Asp Asp Gln Asn Arg Met						
	210			215		220
Val Leu Lys Asn Lys Gly Asn Glu Tyr Glu Lys Gly Lys Arg Gly Asp						
	225			230		235
Leu Tyr Leu Glu Ala Gln Val Lys Glu Asp Glu His Phe Lys Arg Glu						
	245			250		255
Gly Cys Asp Leu Phe Ile Lys Ala Pro Val Phe Phe Thr Thr Ile Ala						
	260			265		270
Leu Gly His Thr Ile Lys Val Pro Ser Leu Lys Gly Asp Glu Leu Glu						
	275			280		285
Leu Lys Ile Pro Arg Asn Ala Arg Asp Lys Gln Thr Phe Ala Phe Arg						
	290			295		300
Asn Glu Gly Val Lys His Pro Glu Ser Ser Tyr Arg Gly Ser Leu Ile						
	305			310		315
Val Glu Leu Gln Val Ile Tyr Pro Lys Ser Leu Asn Lys Glu Gln Gln						
	325			330		335
Glu Leu Leu Glu Lys Leu His Ala Ser Phe Gly Tyr Glu Gly Glu Pro						
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Lys						

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Thr Gln Ile Ala Leu Pro Asn Ser His Pro Leu Leu Lys Lys Val Leu	
15 20 25	
aac tac gcc aaa aag cat ttc agc cag tgc cac atg ctc tct tca tcg	146

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Asn	Tyr	Ala	Lys	Lys	His	Phe	Ser	Gln	Cys	His	Met	Leu	Ser	Ser	Ser			
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Leu	Leu	Ile	Leu	Asn	Asp	Thr	Glu	Cys	Phe	Lys	Lys	Asn	Tyr	Leu	Leu			
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aat	tgg	gtc	tat	cat	gcc	ctt	gaa	tgc	gtg	cat	gaa	aaa	gat	att	agc			242
Asn	Trp	Val	Tyr	His	Ala	Leu	Glu	Cys	Val	His	Glu	Lys	Asp	Ile	Ser			
			65				70						75					
gcg	cat	tct	tta	gaa	gag	gtt	tta	caa	aaa	agc	cac	ctg	ccc	ata	cgc			290
Ala	His	Ser	Leu	Glu	Glu	Val	Leu	Gln	Lys	Ser	His	Leu	Pro	Ile	Arg			
		80					85					90						
atc	aaa	atc	atg	gct	caa	aac	acg	ctt	tta	gaa	aag	ata	gaa	gtg	aaa			338
Ile	Lys	Ile	Met	Ala	Gln	Asn	Thr	Leu	Leu	Glu	Lys	Ile	Glu	Val	Lys			
	95				100					105								
gtt	tta	acc	ttt	ggg	gcg	gaa	tat	gcg	ctt	ttt	atc	acc	aaa	cac	cct			386
Val	Leu	Thr	Phe	Gly	Ala	Glu	Tyr	Ala	Leu	Phe	Ile	Thr	Lys	His	Pro			
110				115				120							125			
atc	gcc	aag	cgg	ttt	tta	cgc	caa	aaa	ttt	agc	ggc	tgt	gtg	ttt	tta			434
Ile	Ala	Lys	Arg	Phe	Leu	Arg	Gln	Lys	Phe	Ser	Gly	Cys	Val	Phe	Leu			
				130				135						140				
gaa	acc	caa	gat	gaa	ttg	cat	ata	aga	ggc	gat	tca	gag	cgt	ttt	tgg			482
Glu	Thr	Gln	Asp	Glu	Leu	His	Ile	Arg	Gly	Asp	Ser	Glu	Arg	Phe	Trp			
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Glu	Leu	Ile	Val	Thr	Leu	Asn	Glu	Asn	Arg	Ile	Val	His	Asn	Ala	Cys			
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Leu	Asp	Phe	Ile	Tyr	Pro	Asn	Gly	Phe	Gly	Lys	Asp	Ser	Tyr	Thr	Thr			
	175					180					185							
atg	gct	gaa	cgc	aaa	tta	aaa	gaa	tgc	tat	aaa	acg	cta	ggg	ttt	atc			626
Met	Ala	Glu	Arg	Lys	Leu	Lys	Glu	Cys	Tyr	Lys	Thr	Leu	Gly	Phe	Ile			
190					195					200				205				
aag	cat	gaa	gat	ttc	agc	gaa	gtc	aaa	aag	cgc	tat	tta	gaa	ttg	gct			674
Lys	His	Glu	Asp	Phe	Ser	Glu	Val	Lys	Lys	Arg	Tyr	Leu	Glu	Leu	Ala			
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aaa	acc	tac	cac	cct	gat	tta	tgc	gat	ctc	aaa	gaa	aaa	aag	gct	ctt			722
Lys	Thr	Tyr	His	Pro	Asp	Leu	Cys	Asp	Leu	Lys	Glu	Lys	Lys	Ala	Leu			
			225					230					235					
tat	gcc	aaa	cgc	ttc	gct	atc	att	caa	gag	gcg	tat	cgc	cac	att	aaa			770
Tyr	Ala	Lys	Arg	Phe	Ala	Ile	Ile	Gln	Glu	Ala	Tyr	Arg	His	Ile	Lys			
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aaa	cac	gcc	taa	accccta	aactagccct	aatcgcgcta	g											810
Lys	His	Ala																
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SECRET

Met 1	Arg	Val	Met	Ala 5	Lys	Ile	Glu	Leu	Leu 10	Ala	Lys	Phe	Thr	Gln 15	Ile
Ala	Leu	Pro	Asn 20	Ser	His	Pro	Leu	Leu 25	Lys	Lys	Val	Leu	Asn 30	Tyr	Ala
Lys	Lys	His 35	Phe	Ser	Gln	Cys	His 40	Met	Leu	Ser	Ser	Ser 45	Leu	Leu	Ile
Leu	Asn 50	Asp	Thr	Glu	Cys	Phe 55	Lys	Lys	Asn	Tyr	Leu 60	Leu	Asn	Trp	Val
Tyr 65	His	Ala	Leu	Glu	Cys 70	Val	His	Glu	Lys	Asp 75	Ile	Ser	Ala	His 80	Ser
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Met	Ala	Gln	Asn 100	Thr	Leu	Leu	Glu	Lys 105	Ile	Glu	Val	Lys	Val 110	Leu	Thr
Phe	Gly	Ala 115	Glu	Tyr	Ala	Leu	Phe 120	Ile	Thr	Lys	His	Pro 125	Ile	Ala	Lys
Arg	Phe 130	Leu	Arg	Gln	Lys	Phe 135	Ser	Gly	Cys	Val	Phe 140	Leu	Glu	Thr	Gln
Asp 145	Glu	Leu	His	Ile 150	Arg	Gly	Asp	Ser	Glu	Arg 155	Phe	Trp	Glu	Leu 160	Ile
Val	Thr	Leu	Asn 165	Glu	Asn	Arg	Ile	Val	His 170	Asn	Ala	Cys	Leu 175	Asp	Phe
Ile	Tyr	Pro 180	Asn	Gly	Phe	Gly	Lys 185	Asp	Ser	Tyr	Thr	Thr 190	Met	Ala	Glu
Arg	Lys	Leu 195	Lys	Glu	Cys	Tyr	Lys 200	Thr	Leu	Gly	Phe 205	Ile	Lys	His	Glu
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His 225	Pro	Asp	Leu	Cys 230	Asp	Leu	Lys	Glu	Lys	Lys 235	Ala	Leu	Tyr	Ala 240	Lys
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Thr	Asp	Ala	Lys	Leu	Ile	Val	Leu	Asn	His	Gln	Ser	Leu	Leu	Asp	Ile		
		65					70					75					
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Ile	Tyr	Leu	Glu	Ala	Tyr	His	Pro	Arg	Asn	Ile	Cys	Trp	Ile	Ala	Lys		
aaa	gag	ctg	ggc	gaa	atc	cct	ttt	tat	ggg	cat	gcc	tta	acg	gat	acc	394	
Lys	Glu	Leu	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	His	Ala	Leu	Thr	Asp	Thr		
gga	atg	att	tta	att	gac	aga	gag	gat	aaa	aag	ggg	att	gtg	agc	ctt	442	
Gly	Met	Ile	Leu	Ile	Asp	Arg	Glu	Asp	Lys	Lys	Gly	Ile	Val	Ser	Leu		
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Leu	Lys	Ala	Cys	Lys	Glu	Lys	Leu	Asp	Gln	Asn	Arg	Pro	Leu	Val	Ile		
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Phe	Pro	Glu	Gly	Thr	Arg	Gly	Lys	Gly	Gly	Glu	Lys	Phe	Leu	Pro	Phe		
aag	caa	ggg	gct	aaa	atc	atc	gcc	gaa	aaa	ttc	cag	ctc	aaa	atc	caa	586	
Lys	Gln	Gly	Ala	Lys	Ile	Ile	Ala	Glu	Lys	Phe	Gln	Leu	Lys	Ile	Gln		
ccc	atg	gtg	tta	atc	aat	tcc	att	aaa	atc	ttt	aat	tcc	aag	cct	cta	634	
Pro	Met	Val	Leu	Ile	Asn	Ser	Ile	Lys	Ile	Phe	Asn	Ser	Lys	Pro	Leu		
gaa	gcc	tat	aaa	gcg	cgc	acc	cgt	tta	gtc	atg	cta	gaa	agc	tat	acg	682	
Glu	Ala	Tyr	Lys	Ala	Arg	Thr	Arg	Leu	Val	Met	Leu	Glu	Ser	Tyr	Thr		
cct	gat	ttt	aac	tcg	ccc	acc	tgg	tat	gaa	gaa	tta	caa	gaa	cgc	atg	730	
Pro	Asp	Phe	Asn	Ser	Pro	Thr	Trp	Tyr	Glu	Glu	Leu	Gln	Glu	Arg	Met		
caa	aaa	gag	tat	tta	aaa	cac	tat	cat	gaa	tta	aac	cct	agc	gaa	caa	778	
Gln	Lys	Glu	Tyr	Leu	Lys	His	Tyr	His	Glu	Leu	Asn	Pro	Ser	Glu	Gln		
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 35 40 45
 Ala Leu Glu Leu Leu Glu Met Thr Gly Ile Glu Cys Val Gln Thr Ile
 50 55 60
 Lys Asp Lys Glu Arg Phe Lys Pro Lys Asp Ala Leu Met Glu Ile Arg
 65 70 75 80
 Gly Asp Phe Ser Met Leu Leu Lys Val Glu Arg Thr Leu Leu Asn Leu
 85 90 95
 Leu Gln His Ser Ser Gly Ile Ala Thr Leu Thr Ser Arg Phe Val Glu
 100 105 110
 Ala Leu Asn Ser His Lys Val Arg Leu Leu Asp Thr Arg Lys Thr Arg
 115 120 125
 Pro Leu Leu Arg Ile Phe Glu Lys Tyr Ser Val Leu Asn Gly Gly Ala
 130 135 140
 Ser Asn His Arg Leu Gly Leu Asp Asp Ala Leu Met Leu Lys Asp Thr
 145 150 155 160
 His Leu Arg His Val Lys Asp Leu Lys Ser Phe Leu Thr His Ala Arg
 165 170 175
 Lys Asn Leu Pro Phe Thr Ala Lys Ile Glu Ile Glu Cys Glu Ser Phe
 180 185 190
 Glu Glu Ala Lys Asn Ala Met Asn Ala Gly Ala Asp Ile Val Met Cys
 195 200 205
 Asp Asn Leu Ser Val Leu Glu Thr Lys Glu Ile Ala Ala Tyr Arg Asp
 210 215 220
 Ala His Tyr Pro Phe Val Leu Leu Glu Ala Ser Gly Asn Ile Ser Leu
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 Lys Ile Ser Leu Asn Ser Asn Lys Arg Ala Trp Met Trp Trp Phe Gln

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ctc tct cgc ctt att cat gat gaa atc aat ttg gag tat ttg aag gcg Leu Ser Arg Leu Ile His Asp Glu Ile Asn Leu Glu Tyr Leu Lys Ala 70 75 80			296
tgc ggg ctc aat ttc ata gaa acg agc gaa aat tta atc acg ctc aaa Cys Gly Leu Asn Phe Ile Glu Thr Ser Glu Asn Leu Ile Thr Leu Lys 85 90 95			344
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gaa acc acc gga tct tgc ccc ata aag cat gag att tta gaa att ggg Glu Thr Thr Gly Ser Cys Pro Ile Lys His Glu Ile Leu Glu Ile Gly 115 120 125 130			440
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act tat gaa gac acc cta aac gcc cca agc gcg cat gaa gct ttg caa Thr Tyr Glu Asp Thr Leu Asn Ala Pro Ser Ala His Glu Ala Leu Gln 165 170 175			584
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gcc att ttg tcc atg cgt tat tct ttg agc ttt tta aaa gag ctt tta Ala Ile Leu Ser Met Arg Tyr Ser Leu Ser Phe Leu Lys Glu Leu Leu 230 235 240			776
ggg ttt ggt ata gaa gtc agc cat aga gcc tat gcg gac gct tta gcg			824

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Ser	Tyr	Lys	Leu	Phe	Glu	Ile	Cys	Leu	Leu	Asn	Leu	Pro	Ser	Tyr	Ile	
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Lys	Thr	Thr	Met	Asp	Leu	Ile	Asp	Phe	Ser	Lys	Cys	Ala	Asn	Thr	Leu	
275					280					285					290	
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Ile	Lys	Arg	Pro	Pro	Lys	Ala	Arg	Tyr	Gln	Glu	Ile	Pro	Ser	Pro	Phe	
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Ser	Leu	Phe	Glu	Lys	Thr	Lys	Gly	Leu	Phe	Asn	His	Lys	Ser	Asn	Gln	
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Leu	Asn	Glu	Ser	Cys	Leu	Met	Gly	Phe	Met	Gly	Thr	Glu	Ile	Leu	Ala	
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Ser	Leu	Phe	Asp	Thr	Phe	Glu	Cys	Cys	Leu	Val	Phe					
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Lys	Ser	Leu	Ser	Arg	Leu	Ile	His	Asp	Glu	Ile	Asn	Leu	Glu	Tyr	Leu	
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Lys	Ala	Cys	Gly	Leu	Asn	Phe	Ile	Glu	Thr	Ser	Glu	Asn	Leu	Ile	Thr	
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Leu	Lys	Asn	Leu	Lys	Thr	Pro	Leu	Lys	Asp	Glu	Val	Phe	Ser	Phe	Ile	
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Asp	Leu	Glu	Thr	Thr	Gly	Ser	Cys	Pro	Ile	Lys	His	Glu	Ile	Leu	Glu	

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 Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu Ser Phe Leu Lys Glu
 225 230 235 240
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 245 250 255
 Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu Leu Asn Leu Pro Ser
 260 265 270
 Tyr Ile Lys Thr Thr Met Asp Leu Ile Asp Phe Ser Lys Cys Ala Asn
 275 280 285
 Thr Leu Ile Lys Arg Pro Pro Lys Ala Arg Tyr Gln Glu Ile Pro Ser
 290 295 300
 Pro Phe Ser Leu Phe Glu Lys Thr Lys Gly Leu Phe Asn His Lys Ser
 305 310 315 320
 Asn Gln Leu Asn Glu Ser Cys Leu Met Gly Phe Met Gly Thr Glu Ile
 325 330 335
 Leu Ala Ser Leu Phe Asp Thr Phe Glu Cys Cys Leu Val Phe
 340 345 350

<210> 189
 <211> 990
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (52)...(864)

<400> 189
 aaaaacactt tttaatgtta taatctatcc taaacaatat aagggggtttt t atg gca 57
 Met Ala
 1
 aaa att gaa agc aat gat tcc cac cta aga ggt att tta aaa gac gaa 105
 Lys Ile Glu Ser Asn Asp Ser His Leu Arg Gly Ile Leu Lys Asp Glu
 5 10 15
 ctc tac tat caa atc ccc atc tac caa cgc cct tat caa tgg aca gaa 153
 Leu Tyr Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp Thr Glu
 20 25 30
 gaa aac tgc gaa aaa ctt tta gac gat ttg ttt ttt aat tat gaa gat 201
 Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr Glu Asp
 35 40 45 50
 gac aga gaa ggc gat tat ttt tgc ggc tca tta gtc tta att gca atc 249
 Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile Ala Ile
 55 60 65
 agc aaa gat tct aaa gcc aca acc tat gat gtt gta gat ggc cag caa 297
 Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly Gln Gln
 70 75 80
 cgc tta agc act ttc att ctg ctt gca aaa gtt tta gcc gat ctt tat 345
 Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp Leu Tyr
 85 90 95

aat gat tgt tta gac cct aag aat tta gaa cat tta caa gag ggt tgg 393
 Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu Gly Trp
 100 105 110

aaa gat agg cat aca gaa aga aaa cga ctg agt ttt aac act ata ggg 441
 Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr Ile Gly
 115 120 125 130

tct aac gct gaa tat gat ttt caa gat gca tta gaa cat ttc aac gac 489
 Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe Asn Asp
 135 140 145

tct caa gca agc aag aat aaa aat aat aag aac aat tac cta aaa aat 537
 Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu Lys Asn
 150 155 160

gcg atc tgt tta aaa gac tat ctc atg aaa aaa gag att aaa aac att 585
 Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys Asn Ile
 165 170 175

aac gat ttc att gag tgg ctg tat tct aat gtt aaa ttt atc acc atc 633
 Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile Thr Ile
 180 185 190

att tgc cca aac ata gac aag gca tta agg att ttt aat gtt tta aac 681
 Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val Leu Asn
 195 200 205 210

gct agg ggt ttg cct ttg aat gcg aca gat att ttt aag ggg gaa tta 729
 Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly Glu Leu
 215 220 225

tta aaa cac gct aaa gag cat gag cga gaa gaa ttt gtg tct cgt tgg 777
 Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser Arg Trp
 230 235 240

aac gcc tta agc caa aaa tgc tcg gac aat gat tta aca atg gag aca 825
 Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met Glu Thr
 245 250 255

tta ttc agt tgg tat aac cta tct caa tcc ggt aac ttc tagagacaaa 874
 Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe
 260 265 270

atggaaaaag agctcggttac ttggttcaac atacttaaca aacccccctt agaatacctt 934
 aagggcgtag aggattttta caacgcttat ggtgaggtgt tagaaatgca agatcg 990

<210> 190
 <211> 271
 <212> PRT
 <213> Helicobacter pylori

<400> 190
 Met Ala Lys Ile Glu Ser Asn Asp Ser His Leu Arg Gly Ile Leu Lys
 1 5 10 15
 Asp Glu Leu Tyr Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp
 20 25 30
 Thr Glu Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr
 35 40 45

Glu Asp Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile
 50 55 60
 Ala Ile Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly
 65 70 75 80
 Gln Gln Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp
 85 90 95
 Leu Tyr Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu
 100 105 110
 Gly Trp Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr
 115 120 125
 Ile Gly Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe
 130 135 140
 Asn Asp Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu
 145 150 155 160
 Lys Asn Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys
 165 170 175
 Asn Ile Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile
 180 185 190
 Thr Ile Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val
 195 200 205
 Leu Asn Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly
 210 215 220
 Glu Leu Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser
 225 230 235 240
 Arg Trp Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met
 245 250 255
 Glu Thr Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe
 260 265 270

<210> 191
 <211> 283
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(230)

<400> 191
 ccctagaatg cgtgcttttg gctaaggaat ttttgcctaa cgctaggcctt atg gtg 56
 Met Val
 1
 gct ggg ggg cgt gaa gtg gtg ttt aaa gat aat gac aaa aag gaa gcc 104
 Ala Gly Gly Arg Glu Val Val Phe Lys Asp Asn Asp Lys Lys Glu Ala
 5 10 15
 aag ctt ttt gaa tac ggc atc aat gcg gtg gtg cta ggg gac tat ttg 152
 Lys Leu Phe Glu Tyr Gly Ile Asn Ala Val Val Leu Gly Asp Tyr Leu
 20 25 30
 acc acc aaa ggc aaa gcc cct aaa aaa gat ata gaa aaa ctg ctc tct 200
 Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu Leu Ser
 35 40 45 50
 tat ggc ttg aca atg gcg aca agc tgt cat taatgagaga acttttttaaa 250
 Tyr Gly Leu Thr Met Ala Thr Ser Cys His
 55 60

agcgtttagag ggttttttcg ccttcttaga atg

283

<210> 192
<211> 60
<212> PRT
<213> Helicobacter pylori

<400> 192
Met Val Ala Gly Gly Arg Glu Val Val Phe Lys Asp Asn Asp Lys Lys
1 5 10 15
Glu Ala Lys Leu Phe Glu Tyr Gly Ile Asn Ala Val Val Leu Gly Asp
20 25 30
Tyr Leu Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu
35 40 45
Leu Ser Tyr Gly Leu Thr Met Ala Thr Ser Cys His
50 55 60

<210> 193
<211> 478
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(425)

<400> 193
cacttggttg gagtgcctat aggcataata agtcctgttt ctatttttaa tgg tgg 56
Trp Trp
1

tat gat aac aat gtc aac tta cag ctt ttt tat gga ttt tta cac aat 104
Tyr Asp Asn Asn Val Asn Leu Gln Leu Phe Tyr Gly Phe Leu His Asn
5 10 15

gtg tat gaa aat gag aag ttt ttc atc ggt tat ttt ata ggg gct ggg 152
Val Tyr Glu Asn Glu Lys Phe Phe Ile Gly Tyr Phe Ile Gly Ala Gly
20 25 30

cta ggg ggt gag agc gta aca ccc aat gtt ctt aaa gat ttt ggt aat 200
Leu Gly Gly Glu Ser Val Thr Pro Asn Val Leu Lys Asp Phe Gly Asn
35 40 45 50

atg tta gcg caa tta gtg caa ttt cag ggc tat ggc tca cta ggg cta 248
Met Leu Ala Gln Leu Val Gln Phe Gln Gly Tyr Gly Ser Leu Gly Leu
55 60 65

agg atg ggc gat aaa cac cac acg cta gaa ttg agc acg agc gtt cat 296
Arg Met Gly Asp Lys His His Thr Leu Glu Leu Ser Thr Ser Val His
70 75 80

ggc gac gct cct agt tgt tct tta aaa aag cta aag agt tgc gaa agt 344
Gly Asp Ala Pro Ser Cys Ser Leu Lys Lys Leu Lys Ser Cys Glu Ser
85 90 95

gcg agg gtt tta caa gca aaa atc cct agg ggc att ttt gaa agc tat 392
Ala Arg Val Leu Gln Ala Lys Ile Pro Arg Gly Ile Phe Glu Ser Tyr
100 105 110

gtt act tgg agc gcg gat tat gtt tat cgt ttt taaaagtttt taaaaattta 445
 Val Thr Trp Ser Ala Asp Tyr Val Tyr Arg Phe
 115 120 125

atggccttgt tccaattgaa taggggtaat aaa 478

<210> 194
 <211> 125
 <212> PRT
 <213> Helicobacter pylori

<400> 194
 Trp Trp Tyr Asp Asn Asn Val Asn Leu Gln Leu Phe Tyr Gly Phe Leu
 1 5 10 15
 His Asn Val Tyr Glu Asn Glu Lys Phe Phe Ile Gly Tyr Phe Ile Gly
 20 25 30
 Ala Gly Leu Gly Gly Glu Ser Val Thr Pro Asn Val Leu Lys Asp Phe
 35 40 45
 Gly Asn Met Leu Ala Gln Leu Val Gln Phe Gln Gly Tyr Gly Ser Leu
 50 55 60
 Gly Leu Arg Met Gly Asp Lys His His Thr Leu Glu Leu Ser Thr Ser
 65 70 75 80
 Val His Gly Asp Ala Pro Ser Cys Ser Leu Lys Lys Leu Lys Ser Cys
 85 90 95
 Glu Ser Ala Arg Val Leu Gln Ala Lys Ile Pro Arg Gly Ile Phe Glu
 100 105 110
 Ser Tyr Val Thr Trp Ser Ala Asp Tyr Val Tyr Arg Phe
 115 120 125

<210> 195
 <211> 2169
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (53)...(2119)

<400> 195
 cttttaaaag gctaatagcct ttttaaaaaa ttgaaataaa ggaataaaaag tt atg acg 58
 Met Thr
 1

gat aac aac caa aac aat gaa aac cat gaa aac agc agt gaa aat tca 106
 Asp Asn Asn Gln Asn Asn Glu Asn His Glu Asn Ser Ser Glu Asn Ser
 5 10 15

aaa gct gat gag atg cga gcc gga gcg ttt gag cgc ttc acc aac cgc 154
 Lys Ala Asp Glu Met Arg Ala Gly Ala Phe Glu Arg Phe Thr Asn Arg
 20 25 30

aaa aag cgt ttc aga gaa aac gcg caa aaa aac gca gag tat tca aac 202
 Lys Lys Arg Phe Arg Glu Asn Ala Gln Lys Asn Ala Glu Tyr Ser Asn
 35 40 45 50

cat gaa gcg tct tcg cac cat aaa aaa gag cat cgc cct aac aaa aaa 250
 His Glu Ala Ser Ser His His Lys Lys Glu His Arg Pro Asn Lys Lys
 55 60 65

SECRET

aat ttg ccc acg gat ttg tat cgt tta gcg cac tat ggc gaa aag ggg Asn Leu Pro Thr Asp Leu Tyr Arg Leu Ala His Tyr Gly Glu Lys Gly 310 315 320	1018
gtg atg ctt ctt tta agc gat tcc acc aac tcc cat aaa tcc ggg act Val Met Leu Leu Leu Ser Asp Ser Thr Asn Ser His Lys Ser Gly Thr 325 330 335	1066
acg ccg agt gaa agc acc ata gcg ccg gct ttt gat acc ctt ttt aaa Thr Pro Ser Glu Ser Thr Ile Ala Pro Ala Phe Asp Thr Leu Phe Lys 340 345 350	1114
gaa gcg caa ggg agg gtg att atg agc acc ttc tct agc aat atc cac Glu Ala Gln Gly Arg Val Ile Met Ser Thr Phe Ser Ser Asn Ile His 355 360 365 370	1162
cgg gtc tat caa gcc ata caa tac ggc att aaa tac aac cgc aag atc Arg Val Tyr Gln Ala Ile Gln Tyr Gly Ile Lys Tyr Asn Arg Lys Ile 375 380 385	1210
gct gtg atc ggg cgc tct atg gaa aaa aac cta gac atc gct aga gaa Ala Val Ile Gly Arg Ser Met Glu Lys Asn Leu Asp Ile Ala Arg Glu 390 395 400	1258
ttg ggc tat atc cat ttg cct tat caa tct ttt att gaa gcc aat gaa Leu Gly Tyr Ile His Leu Pro Tyr Gln Ser Phe Ile Glu Ala Asn Glu 405 410 415	1306
gtc gcc aaa tac ccg gac aat gaa atc tta atc gta acg acc ggc tca Val Ala Lys Tyr Pro Asp Asn Glu Ile Leu Ile Val Thr Thr Gly Ser 420 425 430	1354
caa ggc gaa acc atg agc gcg ctt tat cgc atg gcg act gat gaa cac Gln Gly Glu Thr Met Ser Ala Leu Tyr Arg Met Ala Thr Asp Glu His 435 440 445 450	1402
cgt cat att tct atc aaa ccc aac gat tta gtc atc att tcc gct aaa Arg His Ile Ser Ile Lys Pro Asn Asp Leu Val Ile Ile Ser Ala Lys 455 460 465	1450
gcc att cct ggc aat gaa gcg agc gtt tca gcg gtg ttg aat ttc ttg Ala Ile Pro Gly Asn Glu Ala Ser Val Ser Ala Val Leu Asn Phe Leu 470 475 480	1498
atc aaa aaa gaa gct aaa gtg gct tat caa gaa ttt gac aat atc cat Ile Lys Lys Glu Ala Lys Val Ala Tyr Gln Glu Phe Asp Asn Ile His 485 490 495	1546
gtg agc ggg cat gcc gcc caa gaa gag caa aag ctc atg tta aga ctc Val Ser Gly His Ala Ala Gln Glu Glu Gln Lys Leu Met Leu Arg Leu 500 505 510	1594
att aag cct aag ttt ttc tta ccc gtg cat ggg gaa tat aac cat gtc Ile Lys Pro Lys Phe Phe Leu Pro Val His Gly Glu Tyr Asn His Val 515 520 525 530	1642
gcg cgc cac aaa caa acc gct att tct tgc gga gtg cct gaa aaa aat Ala Arg His Lys Gln Thr Ala Ile Ser Cys Gly Val Pro Glu Lys Asn	1690

09695913.066901

535	540	545	
atc tat tta atg gag gat ggc gat Ile Tyr Leu Met Glu Asp Gly Asp 550	cag gtg gag gtt ggc cct gcg ttc Gln Val Glu Val Gly Pro Ala Phe 555		1738
atc aaa aaa gtc ggc acg att aaa agc ggg aaa agc tat gtg gat aac Ile Lys Lys Val Gly Thr Ile Lys Ser Gly Lys Ser Tyr Val Asp Asn 565			1786
caa agc aat ttg agt att gat aca agc atc gtg caa caa aga gaa gaa Gln Ser Asn Leu Ser Ile Asp Thr Ser Ile Val Gln Gln Arg Glu Glu 580			1834
gtc gct agc gcc ggg gtg ttt gtg gct acg att ttt gtg aat aaa aac Val Ala Ser Ala Gly Val Phe Val Ala Thr Ile Phe Val Asn Lys Asn 595			1882
aag caa gcg ctt tta gaa agc tct caa ttt tcc agt tta ggg ctt gtg Lys Gln Ala Leu Leu Glu Ser Ser Gln Phe Ser Ser Leu Gly Leu Val 615			1930
ggg ttc aaa gat gaa aag cct ttg atc aaa gaa att caa ggg ggc tta Gly Phe Lys Asp Glu Lys Pro Leu Ile Lys Glu Ile Gln Gly Gly Leu 630			1978
gag gtg tta ttg aaa tcc agc aac gcc gaa att ttg aat aac cct aaa Glu Val Leu Leu Lys Ser Ser Asn Ala Glu Ile Leu Asn Asn Pro Lys 645			2026
aaa tta gaa gat cac act cgt aat ttc atc aga aaa gcg ctc ttt aaa Lys Leu Glu Asp His Thr Arg Asn Phe Ile Arg Lys Ala Leu Phe Lys 660			2074
aag ttt aga aaa tac ccg gct atc att tgt cat gcc cat tct ttt Lys Phe Arg Lys Tyr Pro Ala Ile Ile Cys His Ala His Ser Phe 675			2119
tgattgtaac gctattgctt cacaagtttt aaaagatgaa gcgagcgcg			2169
<210> 196			
<211> 689			
<212> PRT			
<213> Helicobacter pylori			
<400> 196			
Met Thr Asp Asn Asn Gln Asn Asn Glu Asn His Glu Asn Ser Ser Glu 1 5 10 15			
Asn Ser Lys Ala Asp Glu Met Arg Ala Gly Ala Phe Glu Arg Phe Thr 20 25 30			
Asn Arg Lys Lys Arg Phe Arg Glu Asn Ala Gln Lys Asn Ala Glu Tyr 35 40 45			
Ser Asn His Glu Ala Ser Ser His His Lys Lys Glu His Arg Pro Asn 50 55 60			
Lys Lys Pro Asn Asn His His Lys Gln Lys His Ala Lys Thr Arg Asn 65 70 75 80			
Tyr Ala Gln Glu Glu Leu Asp Ser Asn Lys Val Glu Gly Val Thr Glu 85 90 95			
Ile Leu His Val Asn Glu Arg Gly Thr Leu Gly Phe His Lys Glu Leu			

		100				105			110
Lys	Lys	Gly	Val	Glu	Ala	Asn	Asn	Lys	Ile
		115					120		Gln
Pro	His	Tyr	Lys	Met	Asn	Leu	Asn	Ser	Lys
		130					135		Ala
Pro	Leu	Gly	Gly	Leu	Gly	Glu	Ile	Gly	Gly
		145				150			Asn
Thr	Pro	Lys	Ser	Ala	Ile	Val	Ile	Asp	Ala
				165				170	Gly
Glu	Gly	Leu	Phe	Gly	Val	Asp	Ile	Leu	Ile
		180						185	Pro
His	Gln	Ile	Lys	Asp	Lys	Ile	Ala	Gly	Ile
		195					200		Ile
Glu	Asp	His	Ile	Gly	Ala	Thr	Pro	Tyr	Leu
		210				215			Phe
Pro	Leu	Tyr	Gly	Thr	Pro	Leu	Ser	Leu	Gly
		225				230			Leu
Asp	Glu	His	Gly	Leu	Lys	Lys	Tyr	Arg	Ser
				245				250	Tyr
Lys	Arg	Cys	Pro	Ile	Ser	Val	Gly	Glu	Phe
		260						265	Ile
Ile	Thr	His	Ser	Ile	Ile	Asp	Ser	Ser	Ala
		275					280		Leu
Ala	Gly	Thr	Ile	Ile	His	Thr	Gly	Asp	Phe
		290				295			Lys
Val	Asp	Asn	Leu	Pro	Thr	Asp	Leu	Tyr	Arg
		305				310			Leu
Lys	Gly	Val	Met	Leu	Leu	Leu	Ser	Asp	Ser
				325				330	Thr
Gly	Thr	Thr	Pro	Ser	Glu	Ser	Thr	Ile	Ala
		340						345	Pro
Phe	Lys	Glu	Ala	Gln	Gly	Arg	Val	Ile	Met
		355					360		Ser
Ile	His	Arg	Val	Tyr	Gln	Ala	Ile	Gln	Tyr
		370				375			Gly
Lys	Ile	Ala	Val	Ile	Gly	Arg	Ser	Met	Glu
		385				390			Lys
Arg	Glu	Leu	Gly	Tyr	Ile	His	Leu	Pro	Tyr
				405				410	Gln
Asn	Glu	Val	Ala	Lys	Tyr	Pro	Asp	Asn	Glu
		420						425	Ile
Gly	Ser	Gln	Gly	Glu	Thr	Met	Ser	Ala	Leu
		435					440		Tyr
Glu	His	Arg	His	Ile	Ser	Ile	Lys	Pro	Asn
		450				455			Asp
Ala	Lys	Ala	Ile	Pro	Gly	Asn	Glu	Ala	Ser
		465				470			Val
Phe	Leu	Ile	Lys	Lys	Glu	Ala	Lys	Val	Ala
				485				490	Tyr
Ile	His	Val	Ser	Gly	His	Ala	Ala	Gln	Glu
		500					505		Glu
Arg	Leu	Ile	Lys	Pro	Lys	Phe	Phe	Leu	Pro
		515					520		Val
His	Val	Ala	Arg	His	Lys	Gln	Thr	Ala	Ile
		530				535			Ser
Lys	Asn	Ile	Tyr	Leu	Met	Glu	Asp	Gly	Asp
		545				550			Gln
Ala	Phe	Ile	Lys	Lys	Val	Gly	Thr	Ile	Lys
				565				570	Ser
									Gly
									Lys
									Ser
									Tyr
									Val

atc acc cca agc aac cac aac aca gaa ggt ttt aaa cat gct tta gac Ile Thr Pro Ser Asn His Asn Thr Glu Gly Phe Lys His Ala Leu Asp 120 125 130	441
gcg ttt aaa gcc atg agc aaa tcc cat aaa ttc gtt ttt gac ttt aaa Ala Phe Lys Ala Met Ser Lys Ser His Lys Phe Val Phe Asp Phe Lys 135 140 145	489
acc caa agc caa gaa tgc aaa gaa ttt atc aaa aac cgt tta aat tct Thr Gln Ser Gln Glu Cys Lys Glu Phe Ile Lys Asn Arg Leu Asn Ser 150 155 160	537
agc cat tta ctc agc aaa atc caa att gac aaa aac aat ttc ttt acg Ser His Leu Leu Ser Lys Ile Gln Ile Asp Lys Asn Asn Phe Phe Thr 165 170 175 180	585
atc tat caa aag tgg ctt gaa att gtc aaa ccc acc att gac ata aat Ile Tyr Gln Lys Trp Leu Glu Ile Val Lys Pro Thr Ile Asp Ile Asn 185 190 195	633
tgg gag gtg gct aaa act aaa gac att tta gac gca gac tat tat tta Trp Glu Val Ala Lys Thr Lys Asp Ile Leu Asp Ala Asp Tyr Tyr Leu 200 205 210	681
gcg gat ttg ctt agc gat ggc gat aaa acc att att gag aaa ttg cac Ala Asp Leu Leu Ser Asp Gly Asp Lys Thr Ile Ile Glu Lys Leu His 215 220 225	729
acg att tta aga tcg agc cat tat aaa ttg aat agg ggt gtg aat gaa Thr Ile Leu Arg Ser Ser His Tyr Lys Leu Asn Arg Gly Val Asn Glu 230 235 240	777
tta ggc aaa atg gat ttt atg gaa gtt ggt ttc aca gac agc caa caa Leu Gly Lys Met Asp Phe Met Glu Val Gly Phe Thr Asp Ser Gln Gln 245 250 255 260	825
gcc cat caa gaa ttt tgg agc gtt tat gaa cga ccg cct aaa aga gaa Ala His Gln Glu Phe Trp Ser Val Tyr Glu Arg Pro Pro Lys Arg Glu 265 270 275	873
ttt caa gcc tct att tta gag cgg cgc gac ttg tta gta cca agc gat Phe Gln Ala Ser Ile Leu Glu Arg Arg Asp Leu Leu Val Pro Ser Asp 280 285 290	921
gtg aga gaa agg aaa ggg gcg ttt ttc acc cct aaa atc tgg gta gaa Val Arg Glu Arg Lys Gly Ala Phe Phe Thr Pro Lys Ile Trp Val Glu 295 300 305	969
aag agt caa gaa tat tta gct aaa gct ttg ggg caa gat tat caa gag Lys Ser Gln Glu Tyr Leu Ala Lys Ala Leu Gly Gln Asp Tyr Gln Glu 310 315 320	1017
gat tgt atc att tgg gat tgc gct ggg ggg act ggg aat ttg ctt cga Asp Cys Ile Ile Trp Asp Cys Ala Gly Gly Thr Gly Asn Leu Leu Arg 325 330 335 340	1065
ggt tta ttg aat aag gct aat ttg tat cta tcc act tta gat cat aac Gly Leu Leu Asn Lys Ala Asn Leu Tyr Leu Ser Thr Leu Asp His Asn 345 350 355	1113

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585										590										595										
gcc	ccc	ttt	gaa	acc	cct	tta	cac	act	ggt	agt	tta	gaa	ata	ttt	gat	1881														
Ala	Pro	Phe	Glu	Thr	Pro	Leu	His	Thr	Val	Ser	Leu	Glu	Ile	Phe	Asp															
			600							605							610													
agt	ttc	ggc	gga	ttt	tta	ggc	agt	aaa	aaa	ata	tac	act	cac	aca	ata	1929														
Ser	Phe	Gly	Gly	Phe	Leu	Gly	Ser	Lys	Lys	Ile	Tyr	Thr	His	Thr	Ile															
			615							620							625													
gac	aaa	atg	ctt	act	tta	gcg	gat	tat	tta	caa	aag	ttt	cag	cca	aca	1977														
Asp	Lys	Met	Leu	Thr	Leu	Ala	Asp	Tyr	Leu	Gln	Lys	Phe	Gln	Pro	Thr															
			630							635							640													
aaa	aga	gac	act	att	ttt	ggc	tat	tta	gat	cct	ggt	cgc	aat	agt	ttt	2025														
Lys	Arg	Asp	Thr	Ile	Phe	Gly	Tyr	Leu	Asp	Pro	Gly	Arg	Asn	Ser	Phe															
			645							650							660													
caa	cat	caa	aat	cta	att	cat	att	agc	att	att	gac	aaa	tca	aaa	caa	2073														
Gln	His	Gln	Asn	Leu	Ile	His	Ile	Ser	Ile	Ile	Asp	Lys	Ser	Lys	Gln															
			665							670							675													
tcg	cat	gta	aaa	tat	ttt	cca	atc	att	gca	act	aca	att	ttg	ttg	gta	2121														
Ser	His	Val	Lys	Tyr	Phe	Pro	Ile	Ile	Ala	Thr	Thr	Ile	Leu	Leu	Val															
			680							685							690													
tct	gta	ttt	ttc	tcc	atc	cgc	cat	tgc	atc	aaa	gcc	aca	tgg	caa	aac	2169														
Ser	Val	Phe	Phe	Ser	Ile	Arg	His	Cys	Ile	Lys	Ala	Thr	Trp	Gln	Asn															
			695							700							705													
gat	agg	gat	caa	ttt	tac	gcc	ccc	tat	gac	gat	gcg	ttc	caa	gac	gac	2217														
Asp	Arg	Asp	Gln	Phe	Tyr	Ala	Pro	Tyr	Asp	Asp	Ala	Phe	Gln	Asp	Asp															
			710							715							720													
agc	gag	ttt	aaa	aac	aat	tgt	ttg	att	ttc	atg	ctt	ttt	cac	acc	cag	2265														
Ser	Glu	Phe	Lys	Asn	Asn	Cys	Leu	Ile	Phe	Met	Leu	Phe	His	Thr	Gln															
			725							730							740													
aac	cgc	atc	act	acc	gct	caa	ggg	act	aac	cat	ttt	atc	ccc	ttt	agc	2313														
Asn	Arg	Ile	Thr	Thr	Ala	Gln	Gly	Thr	Asn	His	Phe	Ile	Pro	Phe	Ser															
			745							750							755													
gaa	act	gaa	gtc	aat	gcc	aaa	gaa	aga	tat	tct	agc	cac	gct	cta	tta	2361														
Glu	Thr	Glu	Val	Asn	Ala	Lys	Glu	Arg	Tyr	Ser	Ser	His	Ala	Leu	Leu															
			760							765							770													
gag	ttt	tta	aaa	ggc	gaa	atc	aaa	gaa	ctt	aaa	gag	aac	gat	agc	ctc	2409														
Glu	Phe	Leu	Lys	Gly	Glu	Ile	Lys	Glu	Leu	Lys	Glu	Asn	Asp	Ser	Leu															
			775							780							785													
ttt	tta	agt	gcc	aaa	aaa	gaa	aac	aag	ccc	ctg	aaa	ttc	agc	ccg	agc	2457														
Phe	Leu	Ser	Ala	Lys	Lys	Glu	Asn	Lys	Pro	Leu	Lys	Phe	Ser	Pro	Ser															
			790							795							800													
gct	tca	aag	gtg	ttt	gac	gct	agc	aga	gag	ggt	tat	cgc	tat	tac	cac	2505														
Ala	Ser	Lys	Val	Phe	Asp	Ala	Ser	Arg	Glu	Val	Tyr	Arg	Tyr	Tyr	His															
			805							810							820													
aca	caa	gat	ttc	aca	aac	cgc	ccc	tat	aac	gct	aac	gca	agc	ctt	tat	2553														

Asp	Ser	Gln	Gln	Ala	His	Gln	Glu	Phe	Trp	Ser	Val	Tyr	Glu	Arg	Pro	
			260					265					270			
Pro	Lys	Arg	Glu	Phe	Gln	Ala	Ser	Ile	Leu	Glu	Arg	Arg	Asp	Leu	Leu	
		275					280					285				
Val	Pro	Ser	Asp	Val	Arg	Glu	Arg	Lys	Gly	Ala	Phe	Phe	Thr	Pro	Lys	
	290					295					300					
Ile	Trp	Val	Glu	Lys	Ser	Gln	Glu	Tyr	Leu	Ala	Lys	Ala	Leu	Gly	Gln	
305					310					315					320	
Asp	Tyr	Gln	Glu	Asp	Cys	Ile	Ile	Trp	Asp	Cys	Ala	Gly	Gly	Thr	Gly	
			325					330						335		
Asn	Leu	Leu	Arg	Gly	Leu	Leu	Asn	Lys	Ala	Asn	Leu	Tyr	Leu	Ser	Thr	
			340					345					350			
Leu	Asp	His	Asn	Asp	Val	Ala	Ile	Val	Lys	Asp	Leu	Ala	Ala	Lys	Asn	
		355					360					365				
His	Leu	Lys	Leu	Leu	Glu	Asn	His	Val	Phe	Gln	Phe	Asp	Phe	Leu	Asn	
	370					375					380					
Asp	Asp	Phe	Phe	Ser	Asp	Lys	Thr	Pro	Lys	Ser	Leu	Gln	Glu	Ile	Leu	
385					390					395					400	
Lys	Asp	Lys	Glu	Lys	Arg	Lys	Lys	Leu	Ile	Ile	Tyr	Ile	Asn	Pro	Pro	
			405					410						415		
Tyr	Ala	Glu	Ala	Gly	Asn	Lys	Ser	Lys	Met	Ser	Gly	Thr	Gly	Glu	His	
			420					425					430			
Lys	Ala	Lys	Val	Ala	Arg	Asp	Asn	Leu	Ile	Cys	Glu	Lys	Tyr	Lys	Asn	
		435					440					445				
Glu	Leu	Gly	Lys	Ala	Asn	Asn	Glu	Val	Phe	Ala	Gln	Phe	Phe	Met	Arg	
	450					455					460					
Ile	Tyr	Lys	Glu	Leu	Asn	Gly	Val	Ile	Leu	Ala	Ser	Phe	Ser	Thr	Leu	
465					470					475					480	
Lys	Asn	Leu	Gln	Gly	Ser	Asn	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Phe	Lys	
			485					490						495		
Ala	Lys	Phe	Leu	Glu	Gly	Phe	Met	Val	Pro	Ala	Asp	Thr	Phe	Asp	Asn	
		500						505					510			
Val	Arg	Gly	Gln	Phe	Pro	Ile	Gly	Phe	Leu	Val	Trp	Asp	Thr	Ser	Ser	
		515					520					525				
Ile	Leu	Pro	Lys	Glu	Asn	Pro	Leu	Asn	Leu	Gly	Gly	Asn	Ser	Lys	Glu	
	530					535					540					
Glu	Lys	Gln	Asn	Ser	Asn	Leu	Ile	Leu	Asp	Gln	Asp	Asn	Leu	Lys	Asp	
545					550					555					560	
Asn	Pro	Leu	Lys	Glu	Arg	Phe	Cys	Leu	Leu	Asp	Ile	Asn	Ala	Pro	Asn	
			565					570						575		
Arg	Lys	Met	Cys	Ser	Gln	Ser	Arg	Thr	Arg	Thr	Lys	Gly	Thr	Gln	Lys	
		580						585					590			
His	Ser	Thr	Ala	Ala	Pro	Phe	Glu	Thr	Pro	Leu	His	Thr	Val	Ser	Leu	
		595					600					605				
Glu	Ile	Phe	Asp	Ser	Phe	Gly	Gly	Phe	Leu	Gly	Ser	Lys	Lys	Ile	Tyr	
	610					615					620					
Thr	His	Thr	Ile	Asp	Lys	Met	Leu	Thr	Leu	Ala	Asp	Tyr	Leu	Gln	Lys	
625					630					635					640	
Phe	Gln	Pro	Thr	Lys	Arg	Asp	Thr	Ile	Phe	Gly	Tyr	Leu	Asp	Pro	Gly	
			645					650						655		
Arg	Asn	Ser	Phe	Gln	His	Gln	Asn	Leu	Ile	His	Ile	Ser	Ile	Ile	Asp	
			660					665					670			
Lys	Ser	Lys	Gln	Ser	His	Val	Lys	Tyr	Phe	Pro	Ile	Ile	Ala	Thr	Thr	
		675					680					685				
Ile	Leu	Leu	Val	Ser	Val	Phe	Phe	Ser	Ile	Arg	His	Cys	Ile	Lys	Ala	
	690					695					700					
Thr	Trp	Gln	Asn	Asp	Arg	Asp	Gln	Phe	Tyr	Ala	Pro	Tyr	Asp	Asp	Ala	
705					710					715					720	
Phe	Gln	Asp	Asp	Ser	Glu	Phe	Lys	Asn	Asn	Cys	Leu	Ile	Phe	Met	Leu	

				725						730					735				
Phe	His	Thr	Gln	Asn	Arg	Ile	Thr	Thr	Ala	Gln	Gly	Thr	Asn	His	Phe				
			740						745					750					
Ile	Pro	Phe	Ser	Glu	Thr	Glu	Val	Asn	Ala	Lys	Glu	Arg	Tyr	Ser	Ser				
		755						760					765						
His	Ala	Leu	Leu	Glu	Phe	Leu	Lys	Gly	Glu	Ile	Lys	Glu	Leu	Lys	Glu				
	770					775					780								
Asn	Asp	Ser	Leu	Phe	Leu	Ser	Ala	Lys	Lys	Glu	Asn	Lys	Pro	Leu	Lys				
785					790					795				800					
Phe	Ser	Pro	Ser	Ala	Ser	Lys	Val	Phe	Asp	Ala	Ser	Arg	Glu	Val	Tyr				
				805					810					815					
Arg	Tyr	Tyr	His	Thr	Gln	Asp	Phe	Thr	Asn	Arg	Pro	Tyr	Asn	Ala	Asn				
			820					825					830						
Ala	Ser	Leu	Tyr	Asp	Ile	Lys	Glu	Phe	Phe	Gln	Gly	Arg	Asn	Lys	Gln				
		835					840					845							
Gly	Lys	Leu	Asn	Leu	Pro	Ala	Lys	Ala	Lys	Asp	Glu	Tyr	Tyr	Lys	Gln				
	850					855				860									
Leu	Tyr	Ala	Asn	Leu	Gln	Asp	Ala	Leu	Lys	Asp	Leu	Ala	Lys	Glu	Ile				
865					870					875				880					
Gln	Pro	Lys	Val	Tyr	Glu	Tyr	Gly	Phe	Leu	Arg	Glu								
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 <213> Helicobacter pylori

<220>
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gagataaaag atg tta gaa ttt att tta aaa att caa gct aga gac tct aaa	111
Met Leu Glu Phe Ile Leu Lys Ile Gln Ala Arg Asp Ser Lys	
1 5 10	
ggc ttg gtg agc acg att agc acc act atc gct aac aag ggc tat aac	159
Gly Leu Val Ser Thr Ile Ser Thr Thr Ile Ala Asn Lys Gly Tyr Asn	
15 20 25 30	
atc gtc aaa aac gat gaa ttt gtt gat ccc tta aaa cag cgt ttt ttc	207
Ile Val Lys Asn Asp Glu Phe Val Asp Pro Leu Lys Gln Arg Phe Phe	
35 40 45	
atg cgg tta aaa atc caa aaa gaa atc aag ccc ttg aat act gaa att	255
Met Arg Leu Lys Ile Gln Lys Glu Ile Lys Pro Leu Asn Thr Glu Ile	
50 55 60	
aaa gag caa gaa gag caa tcc tta aag acc gct ctt ttt aaa gcc cta	303
Lys Glu Gln Glu Glu Gln Ser Leu Lys Thr Ala Leu Phe Lys Ala Leu	
65 70 75	
gaa aac ttt aac gag tta ttg att gaa gtc att tta acg cat aaa aaa	351
Glu Asn Phe Asn Glu Leu Leu Ile Glu Val Ile Leu Thr His Lys Lys	
80 85 90	
aac atc att ctg ctc gct act aaa gag agc cat tgc tta ggg gat ttg	399
Asn Ile Ile Leu Leu Ala Thr Lys Glu Ser His Cys Leu Gly Asp Leu	

0585913-062901

95	100	105	110	
ctt tta agg gtg tat ggg ggg gaa ttg aac gct caa att tta ggc gtt	Leu Leu Arg Val Tyr 115	Gly Gly Glu Leu Asn Ala Gln Ile Leu Gly Val 120		447
att tcc aac cac gag att tta cgc cct tta gtg gaa aaa ttt gac atc	Ile Ser Asn His 130	Glu Ile Leu Arg Pro Leu Val Glu Lys Phe Asp Ile 135		495
cct tat ttt tat gcg cct tgc gac aat caa gtt ttg cat gaa aaa gaa	Pro Tyr Phe Tyr 145	Ala Pro Cys Asp Asn Gln Val Leu His Glu Lys Glu 150		543
gtt tta gaa atc att aaa aac ctg gaa tta aag cac aaa gtg agt gca	Val Leu Glu Ile Ile Lys Asn Leu Glu Leu Lys His Lys Val Ser Ala 160			591
gac ttg ctc gtt tta gcc aaa tac atg cgc att tta agc cat gat ttt	Asp Leu Leu Val Leu Ala Lys Tyr Met Arg Ile Leu Ser His Asp Phe 175			639
acg aag cgc tat gaa aac cag atc tta aat atc cat cat agt ttc ttg	Thr Lys Arg Tyr Glu Asn Gln Ile Leu Asn Ile His His Ser Phe Leu 195			687
ccc gca ttc att ggg gct aat cct tac cag caa gcg ttt gaa agg ggc	Pro Ala Phe Ile Gly Ala Asn Pro Tyr Gln Gln Ala Phe Glu Arg Gly 210			735
gtg aaa gtc atc ggg gcc acg gcg cat ttt gtg aat gaa agc ctt gat	Val Lys Val Ile Gly Ala Thr Ala His Phe Val Asn Glu Ser Leu Asp 225			783
gct ggg ccg att atc ata caa gac act ctg ccc att aac cac aat tac	Ala Gly Pro Ile Ile Ile Gln Asp Thr Leu Pro Ile Asn His Asn Tyr 240			831
agc gtg gaa aaa atg cgc cta gcg ggt aag gat ata gaa aaa ctg gtt	Ser Val Glu Lys Met Arg Leu Ala Gly Lys Asp Ile Glu Lys Leu Val 255			879
tta gct agg gct tta aaa ctc gtt tta gaa gac aga gtc ttt gta cat	Leu Ala Arg Ala Leu Lys Leu Val Leu Glu Asp Arg Val Phe Val His 275			927
gaa aat aaa acg gtg gtg ttt tgaatgcttt tagatttcag caacctcaat				978
Glu Asn Lys Thr Val Val Phe 290				
gaagaaccct taataaac				996
<210> 200				
<211> 293				
<212> PRT				
<213> Helicobacter pylori				
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Asp	Pro	Thr	Leu	Pro	Ala	Trp	Val	Tyr	Ser	Val	Ala	Leu	Leu	Lys	Val	
				40					45					50		
tat	ttt	agc	gat	ggg	act	tat	aaa	gaa	ggc	tat	gcg	act	ttg	ctc	aaa	248
Tyr	Phe	Ser	Asp	Gly	Thr	Tyr	Lys	Glu	Gly	Tyr	Ala	Thr	Leu	Leu	Lys	
				55				60					65			
aac	ggg	cgt	tat	atc	gct	tct	tct	gaa	acg	ctt	tat	tct	aac	ggc	tta	296
Asn	Gly	Arg	Tyr	Ile	Ala	Ser	Ser	Glu	Thr	Leu	Tyr	Ser	Asn	Gly	Leu	
		70					75					80				
tac	cct	aaa	acg	att	tta	gcc	aaa	atg	caa	gac	agc	agc	gct	aaa	gag	344
Tyr	Pro	Lys	Thr	Ile	Leu	Ala	Lys	Met	Gln	Asp	Ser	Ser	Ala	Lys	Glu	
		85				90					95					
ctg	att	tgt	ata	gct	agc	cta	cgc	ctt	gaa	gcg	atg	gat	agg	aat	caa	392
Leu	Ile	Cys	Ile	Ala	Ser	Leu	Arg	Leu	Glu	Ala	Met	Asp	Arg	Asn	Gln	
100				105						110					115	
ggg	ctt	tcg	ctt	tta	aaa	acc	gcc	gat	ttt	aga	gac	gat	tat	tgc	cat	440
Gly	Leu	Ser	Leu	Leu	Lys	Thr	Ala	Asp	Phe	Arg	Asp	Asp	Tyr	Cys	His	
				120					125					130		
aaa	aga	gaa	gag	agc	tat	tat	cat	gca	agg	att	tac	aca	aaa	tac	gct	488
Lys	Arg	Glu	Glu	Ser	Tyr	Tyr	His	Ala	Arg	Ile	Tyr	Thr	Lys	Tyr	Ala	
			135					140					145			
caa	act	ttt	cat	tca	aat	ccc	tat	acc	aat	caa	aaa	aca	ccc	aat	tct	536
Gln	Thr	Phe	His	Ser	Asn	Pro	Tyr	Thr	Asn	Gln	Lys	Thr	Pro	Asn	Ser	
		150					155					160				
gat	ctc	tac	tac	cca	gcg	tta	aat	gag	ggg	aat	tct	ttt	tct	ata	cag	584
Asp	Leu	Tyr	Tyr	Pro	Ala	Leu	Asn	Glu	Gly	Asn	Ser	Phe	Ser	Ile	Gln	
						170					175					
ata	atg	ggc	att	tct	gtg	gct	gaa	ctt	ttg	aaa	tct	aaa	aaa	ttc	ctt	632
Ile	Met	Gly	Ile	Ser	Val	Ala	Glu	Leu	Leu	Lys	Ser	Lys	Lys	Phe	Leu	
180					185					190					195	
tcg	ctt	gat	gtt	tct	ttt	aaa	aag	ggg	agc	gtg	ttg	tgg	gga	ggg	agg	680
Ser	Leu	Asp	Val	Ser	Phe	Lys	Lys	Gly	Ser	Val	Leu	Trp	Gly	Gly	Arg	
				200					205					210		
cct	tat	ttt	agc	gaa	gtg	ggg	gag	ttt	atg	ggg	atg	gct	agc	agc	act	728
Pro	Tyr	Phe	Ser	Glu	Val	Gly	Glu	Phe	Met	Gly	Met	Ala	Ser	Ser	Thr	
			215					220					225			
tta	gaa	aac	caa	gaa	agt	ctg	gtg	att	atc	cct	aaa	gaa	aag	atc	gtg	776
Leu	Glu	Asn	Gln	Glu	Ser	Leu	Val	Ile	Ile	Pro	Lys	Glu	Lys	Ile	Val	
		230					235					240				
caa	ttt	tta	aac	gct	cta	aaa	aat	caa	aat	att	ttc	cca	aac	att	ccc	8

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 <212> PRT
 <213> Helicobacter pylori

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 20 25 30
 Pro Pro Leu Asp Pro Thr Leu Pro Ala Trp Val Tyr Ser Val Ala Leu
 35 40 45
 Leu Lys Val Tyr Phe Ser Asp Gly Thr Tyr Lys Glu Gly Tyr Ala Thr
 50 55 60
 Leu Leu Lys Asn Gly Arg Tyr Ile Ala Ser Ser Glu Thr Leu Tyr Ser
 65 70 75 80
 Asn Gly Leu Tyr Pro Lys Thr Ile Leu Ala Lys Met Gln Asp Ser Ser
 85 90 95
 Ala Lys Glu Leu Ile Cys Ile Ala Ser Leu Arg Leu Glu Ala Met Asp
 100 105 110
 Arg Asn Gln Gly Leu Ser Leu Leu Lys Thr Ala Asp Phe Arg Asp Asp
 115 120 125
 Tyr Cys His Lys Arg Glu Glu Ser Tyr Tyr His Ala Arg Ile Tyr Thr
 130 135 140
 Lys Tyr Ala Gln Thr Phe His Ser Asn Pro Tyr Thr Asn Gln Lys Thr
 145 150 155 160
 Pro Asn Ser Asp Leu Tyr Tyr Pro Ala Leu Asn Glu Gly Asn Ser Phe
 165 170 175
 Ser Ile Gln Ile Met Gly Ile Ser Val Ala Glu Leu Leu Lys Ser Lys
 180 185 190
 Lys Phe Leu Ser Leu Asp Val Ser Phe Lys Lys Gly Ser Val Leu Trp
 195 200 205
 Gly Gly Arg Pro Tyr Phe Ser Glu Val Gly Glu Phe Met Gly Met Ala
 210 215 220
 Ser Ser Thr Leu Glu Asn Gln Glu Ser Leu Val Ile Ile Pro Lys Glu
 225 230 235 240
 Lys Ile Val Gln Phe Leu Asn Ala Leu Lys Asn Gln Asn Ile Phe Pro
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 Asn Ile Pro

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 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (88)...(603)

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 Met Phe Asp Lys Lys Leu Ser Ser Asn
 1 5
 gat tgg cat atc caa aaa gtg gaa atg aac cat caa gtc tat gac att 162
 Asp Trp His Ile Gln Lys Val Glu Met Asn His Gln Val Tyr Asp Ile
 10 15 20 25

gaa acc atg ctc gct gat agc gct ttt aga gag cat gaa gaa gag caa 210
 Glu Thr Met Leu Ala Asp Ser Ala Phe Arg Glu His Glu Glu Glu Gln
 30 35 40

gat tcc tct cta aat acc gct ttg cct gaa gat aaa aca gcg att gaa 258
 Asp Ser Ser Leu Asn Thr Ala Leu Pro Glu Asp Lys Thr Ala Ile Glu
 45 50 55

gcc aaa gag caa gag caa aaa gaa aaa aga aaa cgc tgg tat gag ctt 306
 Ala Lys Glu Gln Glu Gln Lys Glu Lys Arg Lys Arg Trp Tyr Glu Leu
 60 65 70

ttt aaa aag aaa cca aag ccc aaa agc tct atg gga gag ttt gtg ttt 354
 Phe Lys Lys Lys Pro Lys Pro Lys Ser Ser Met Gly Glu Phe Val Phe
 75 80 85

gat caa aaa gaa aat cgt att tat ggc aaa ggc tat tgc aac cgg tat 402
 Asp Gln Lys Glu Asn Arg Ile Tyr Gly Lys Gly Tyr Cys Asn Arg Tyr
 90 95 100 105

ttt gcc agc tat gta tgg cag ggc gat agg cac att ggg att gaa gat 450
 Phe Ala Ser Tyr Val Trp Gln Gly Asp Arg His Ile Gly Ile Glu Asp
 110 115 120

agc ggg att tca aga aaa gtg tgt aaa gat gag cat tta atg gcg ttt 498
 Ser Gly Ile Ser Arg Lys Val Cys Lys Asp Glu His Leu Met Ala Phe
 125 130 135

gaa ttg gaa ttt atg gag aat ttt aag ggt aat ttt acg gta act aag 546
 Glu Leu Glu Phe Met Glu Asn Phe Lys Gly Asn Phe Thr Val Thr Lys
 140 145 150

ggc aag gac acg ctc att tta gac aac caa aaa atg aaa att tat ttg 594
 Gly Lys Asp Thr Leu Ile Leu Asp Asn Gln Lys Met Lys Ile Tyr Leu
 155 160 165

aaa acg cct tgagtggggtt tttgatttca aaacaatcta agatcactaa 643
 Lys Thr Pro
 170

attagggtt aaaaagaaat ttttaa 669

<210> 204
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 <213> Helicobacter pylori

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 20 25 30
 Ala Phe Arg Glu His Glu Glu Glu Gln Asp Ser Ser Leu Asn Thr Ala
 35 40 45
 Leu Pro Glu Asp Lys Thr Ala Ile Glu Ala Lys Glu Gln Glu Gln Lys
 50 55 60
 Glu Lys Arg Lys Arg Trp Tyr Glu Leu Phe Lys Lys Lys Pro Lys Pro
 65 70 75 80

Lys Ser Ser Met Gly Glu Phe Val Phe Asp Gln Lys Glu Asn Arg Ile
85 90 95
Tyr Gly Lys Gly Tyr Cys Asn Arg Tyr Phe Ala Ser Tyr Val Trp Gln
100 105 110
Gly Asp Arg His Ile Gly Ile Glu Asp Ser Gly Ile Ser Arg Lys Val
115 120 125
Cys Lys Asp Glu His Leu Met Ala Phe Glu Leu Glu Phe Met Glu Asn
130 135 140
Phe Lys Gly Asn Phe Thr Val Thr Lys Gly Lys Asp Thr Leu Ile Leu
145 150 155 160
Asp Asn Gln Lys Met Lys Ile Tyr Leu Lys Thr Pro
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<212> DNA
<213> Helicobacter pylori

<220>
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<222> (53)...(235)

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Ile Asn
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ttg acg cta acc cct ata aaa cga ttt ttg gag aaa gga aat aat cat 106
Leu Thr Leu Thr Pro Ile Lys Arg Phe Leu Glu Lys Gly Asn Asn His
5 10 15

gag agc tac ggc gat aaa aat ctt ttc act ctc atc agc att agc cct 154
Glu Ser Tyr Gly Asp Lys Asn Leu Phe Thr Leu Ile Ser Ile Ser Pro
20 25 30

att gct tca tgg ttg ctt gag cat caa ttt aaa aca aat gct acc aga 202
Ile Ala Ser Trp Leu Leu Glu His Gln Phe Lys Thr Asn Ala Thr Arg
35 40 45 50

gat cag aac tta cga ttt gaa tgc gag ttc ttt tgaaatcacg caatgcgcta 255
Asp Gln Asn Leu Arg Phe Glu Cys Glu Phe Phe
55 60

aacctttgac tgaagtgagg ctcattagta ttttg 290

<210> 206
<211> 61
<212> PRT
<213> Helicobacter pylori

<400> 206
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Asn His Glu Ser Tyr Gly Asp Lys Asn Leu Phe Thr Leu Ile Ser Ile
20 25 30
Ser Pro Ile Ala Ser Trp Leu Leu Glu His Gln Phe Lys Thr Asn Ala
35 40 45
Thr Arg Asp Gln Asn Leu Arg Phe Glu Cys Glu Phe Phe
50 55 60

Station	Time	Lat.	Long.	Depth	Temp.	Wind	Wave	Clouds	Remarks
1	0800	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
2	0900	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
3	1000	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
4	1100	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
5	1200	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
6	1300	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
7	1400	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
8	1500	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
9	1600	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
10	1700	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
11	1800	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
12	1900	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
13	2000	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
14	2100	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
15	2200	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
16	2300	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
17	0000	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
18	0100	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
19	0200	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
20	0300	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
21	0400	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
22	0500	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
23	0600	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear
24	0700	34° 15' N	122° 05' W	10	55.5	15	2	100	Clear

<400> 207																
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Met Leu Lys Arg Met Ile Leu Leu Gly																
1 5																
gct	ttg	ggt	gtt	tta	gcg	agc	gct	gaa	gag	agt	gcg	gct	ttt	gtg	gga	102
Ala	Leu	Gly	Val	Leu	Ala	Ser	Ala	Glu	Glu	Ser	Ala	Ala	Phe	Val	Gly	
10					15					20					25	
gtc	aat	tac	cag	gtg	agc	atg	ata	caa	aat	cag	act	aaa	atg	gtg	aat	150
Val	Asn	Tyr	Gln	Val	Ser	Met	Ile	Gln	Asn	Gln	Thr	Lys	Met	Val	Asn	
				30					35					40		
gac	aac	ggc	ttg	caa	aag	cct	ttg	ata	aag	ttt	ccg	cct	tac	gca	gga	198
Asp	Asn	Gly	Leu	Gln	Lys	Pro	Leu	Ile	Lys	Phe	Pro	Pro	Tyr	Ala	Gly	
			45					50					55			
gcg	ggt	ttt	gaa	gtg	ggc	tat	aag	caa	ttt	ttt	ggt	aag	aaa	aaa	tgg	246
Ala	Gly	Phe	Glu	Val	Gly	Tyr	Lys	Gln	Phe	Phe	Gly	Lys	Lys	Lys	Trp	
		60					65					70				
ttt	ggc	atg	cgt	tat	tat	ggg	ttt	ttt	gac	tac	gcg	cac	aac	cgc	ttt	294
Phe	Gly	Met	Arg	Tyr	Tyr	Gly	Phe	Phe	Asp	Tyr	Ala	His	Asn	Arg	Phe	
	75					80					85					
ggc	gtg	atg	aaa	aag	ggc	att	ccg	gtg	ggc	gat	agt	ggg	ttt	att	tac	342
Gly	Val	Met	Lys	Lys	Gly	Ile	Pro	Val	Gly	Asp	Ser	Gly	Phe	Ile	Tyr	
	90				95					100					105	
aat	agt	ttt	agt	ttt	gga	ggg	aac	act	tta	acg	gaa	agg	gat	tcc	tat	390
Asn	Ser	Phe	Ser	Phe	Gly	Gly	Asn	Thr	Leu	Thr	Glu	Arg	Asp	Ser	Tyr	
				110					115					120		
cag	ggg	caa	tac	tat	gtc	aat	tta	ttc	act	tat	ggc	gtg	ggg	tta	gat	438
Gln	Gly	Gln	Tyr	Tyr	Val	Asn	Leu	Phe	Thr	Tyr	Gly	Val	Gly	Leu	Asp	
			125					130					135			
acg	ctg	tgg	aat	ttt	gtg	aat	aaa	gaa	aac	atg	gtt	ttt	ggt	ttt	gtg	486
Thr	Leu	Trp	Asn	Phe	Val	Asn	Lys	Glu	Asn	Met	Val	Phe	Gly	Phe	Val	
		140					145					150				
gtg	ggg	atc	caa	tta	gcg	ggg	gat	agt	tgg	gca	acg	agc	atc	agt	aaa	534
Val	Gly	Ile	Gln	Leu	Ala	Gly	Asp	Ser	Trp	Ala	Thr	Ser	Ile	Ser	Lys	
	155					160					165					
gaa	atc	gct	cat	tat	gca	aaa	cac	cac	agc	aat	tcc	agt	tat	agc	ccg	582
Glu	Ile	Ala	His	Tyr	Ala	Lys	His	His	Ser	Asn	Ser	Ser	Tyr	Ser	Pro	
	170				175					180					185	
gcc	aat	ttc	cag	ttt	tta	tgg	aag	ttt	ggg	gtc	cgc	acc	cat	atc	gct	630

Ala	Asn	Phe	Gln	Phe	Leu	Trp	Lys	Phe	Gly	Val	Arg	Thr	His	Ile	Ala	
				190					195					200		
aaa	cac	aat	agc	cta	gaa	tta	ggg	att	aaa	gtg	cct	acg	atc	aca	cac	678
Lys	His	Asn	Ser	Leu	Glu	Leu	Gly	Ile	Lys	Val	Pro	Thr	Ile	Thr	His	
			205				210						215			
cag	ctt	ttc	tct	ctt	acc	aac	gaa	aag	gga	tac	acc	tta	cag	gct	gat	726
Gln	Leu	Phe	Ser	Leu	Thr	Asn	Glu	Lys	Gly	Tyr	Thr	Leu	Gln	Ala	Asp	
		220					225					230				
gtg	cgt	aga	ggt	tat	gcg	ttt	caa	atc	agt	tac	ttg	agg	gat	ttt		771
Val	Arg	Arg	Val	Tyr	Ala	Phe	Gln	Ile	Ser	Tyr	Leu	Arg	Asp	Phe		
	235					240					245					
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<210> 208
 <211> 248
 <212> PRT
 <213> Helicobacter pylori

<400> 208															
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Ala	Glu	Glu	Ser	Ala	Ala	Phe	Val	Gly	Val	Asn	Tyr	Gln	Val	Ser	Met
			20					25					30		
Ile	Gln	Asn	Gln	Thr	Lys	Met	Val	Asn	Asp	Asn	Gly	Leu	Gln	Lys	Pro
		35				40						45			
Leu	Ile	Lys	Phe	Pro	Pro	Tyr	Ala	Gly	Ala	Gly	Phe	Glu	Val	Gly	Tyr
	50					55					60				
Lys	Gln	Phe	Phe	Gly	Lys	Lys	Lys	Trp	Phe	Gly	Met	Arg	Tyr	Tyr	Gly
65					70					75					80
Phe	Phe	Asp	Tyr	Ala	His	Asn	Arg	Phe	Gly	Val	Met	Lys	Lys	Gly	Ile
				85					90					95	
Pro	Val	Gly	Asp	Ser	Gly	Phe	Ile	Tyr	Asn	Ser	Phe	Ser	Phe	Gly	Gly
			100					105					110		
Asn	Thr	Leu	Thr	Glu	Arg	Asp	Ser	Tyr	Gln	Gly	Gln	Tyr	Tyr	Val	Asn
	115					120						125			
Leu	Phe	Thr	Tyr	Gly	Val	Gly	Leu	Asp	Thr	Leu	Trp	Asn	Phe	Val	Asn
	130					135					140				
Lys	Glu	Asn	Met	Val	Phe	Gly	Phe	Val	Val	Gly	Ile	Gln	Leu	Ala	Gly
145					150					155					160
Asp	Ser	Trp	Ala	Thr	Ser	Ile	Ser	Lys	Glu	Ile	Ala	His	Tyr	Ala	Lys
			165						170					175	
His	His	Ser	Asn	Ser	Ser	Tyr	Ser	Pro	Ala	Asn	Phe	Gln	Phe	Leu	Trp
			180					185					190		
Lys	Phe	Gly	Val	Arg	Thr	His	Ile	Ala	Lys	His	Asn	Ser	Leu	Glu	Leu
		195					200					205			
Gly	Ile	Lys	Val	Pro	Thr	Ile	Thr	His	Gln	Leu	Phe	Ser	Leu	Thr	Asn
	210					215					220				
Glu	Lys	Gly	Tyr	Thr	Leu	Gln	Ala	Asp	Val	Arg	Arg	Val	Tyr	Ala	Phe
225					230					235					240
Gln	Ile	Ser	Tyr	Leu	Arg	Asp	Phe								
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<210> 209
 <211> 1354
 <212> DNA

SECRET

<221> CDS

<400> 209

-237-

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 50 55 60
 Ser Ile Ser Ala Ile Leu Gln Phe Ile Leu Lys Pro Leu Thr Trp Gly
 65 70 75 80
 Leu Gly Ser Thr Thr Glu Ser Ile Ala Glu Phe Lys Phe Ser Leu Pro
 85 90 95
 Leu Lys Pro Thr Ala Asn Ala Gln Thr Leu Glu Asp Ile Asp Phe Asp
 100 105 110
 Phe Met Glu Lys Phe Ile Ala Glu Leu Glu Gln Cys Arg Leu Ala Glu
 115 120 125
 Leu Glu Gln Cys Arg Leu Ala Glu Leu Gln Ala Tyr Leu Lys Ala Thr
 130 135 140
 Gly Leu Glu Asn Thr Thr Leu Ser Asn Asp Glu Glu Asn Ala Leu Asn
 145 150 155 160
 Val Phe Asn Asn Ser Gly Gly Gly Gly Gly Asn Thr Pro Cys Gly Leu
 165 170 175
 Thr Trp Gln Ser Phe Arg Leu Gly Asp Leu Phe Glu Ile Glu Lys Thr
 180 185 190
 Leu Ser Phe Asn Lys Asp Ala Leu Thr Gln Gly Glu Asp Tyr Asp Tyr
 195 200 205
 Ile Thr Arg Thr Ser Gln Asn Gln Gly Val Leu Gln Thr Thr Gly Phe
 210 215 220
 Val Asn Ala Glu Asn Leu Asn Pro Pro Phe Thr Trp Ser Leu Gly Leu
 225 230 235 240
 Leu Gln Met Asp Phe Phe Tyr Arg Lys Lys Ser Trp Tyr Ala Gly Gln
 245 250 255
 Phe Met Arg Lys Ile Thr Pro Lys Thr Glu Ile Glu Asn Lys Ile Asp
 260 265 270
 Leu Arg Ile Ala Asn Tyr Phe Thr Thr Leu Leu Asn Ala Leu Lys Arg
 275 280 285
 Pro Leu Leu Ser Val Leu Val Arg Asp Ile Asp Lys Thr Phe Arg Glu
 290 295 300
 Gln Lys Ile Gln Leu Pro Leu Lys Pro Thr Ala Lys Thr Gln Thr Leu
 305 310 315 320
 Asp Gly Ile Asp Phe Asp Phe Met His Thr Leu Ile Asn Ala Leu Met
 325 330 335
 Lys Gln Thr Ile Gln Gly Val Ala Gln Tyr Cys Asp Ala Lys Ile Gln
 340 345 350
 Ala Thr Lys Glu Val Ile Ser Gln Glu Ala Pro Val Gln Lys Asp Ser
 355 360 365
 Leu Phe
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 <212> DNA
 <213> Helicobacter pylori

<220>
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 ttaagtcgta ttctgcgcta atctcgccca tgatctcttc aatgatgtct tccatagtga 120
 gcaacccggc tgtgcccggc tattcatcaa tcaccaaagc ggt atg gat ttg ctc 175
 Met Asp Leu Leu

ttt ttt cat ttt aat aag gat ttg aga aat gga agc gct ttc ggg gac 223
 Phe Phe His Phe Asn Lys Asp Leu Arg Asn Gly Ser Ala Phe Gly Asp
 5 10 15 20

gat gat cat ttt cct aac gat ttg att gaa atc atg cat ttt ggg ggt 271
 Asp Asp His Phe Pro Asn Asp Leu Ile Glu Ile Met His Phe Gly Gly
 25 30 35

aaa aat aga gcg cga aag caa atc cct aat atg cac cat gcc gat aat 319
 Lys Asn Arg Ala Arg Lys Gln Ile Pro Asn Met His His Ala Asp Asn
 40 45 50

gtt atc ctt aga acc ctt gca ata agg gta gcg cgt gaa atg gcc ttt 367
 Val Ile Leu Arg Thr Leu Ala Ile Arg Val Ala Arg Glu Met Ala Phe
 55 60 65

taaaacaatg tctatatatttt cttcatagct gttttcttca tccaaacaca ccatgtcttt 427
 tcgtgggggc atgatttctt tag 450

<210> 212
 <211> 68
 <212> PRT
 <213> Helicobacter pylori

<400> 212
 Met Asp Leu Leu Phe Phe His Phe Asn Lys Asp Leu Arg Asn Gly Ser
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 Ala Phe Gly Asp Asp Asp His Phe Pro Asn Asp Leu Ile Glu Ile Met
 20 25 30
 His Phe Gly Gly Lys Asn Arg Ala Arg Lys Gln Ile Pro Asn Met His
 35 40 45
 His Ala Asp Asn Val Ile Leu Arg Thr Leu Ala Ile Arg Val Ala Arg
 50 55 60
 Glu Met Ala Phe
 65

<210> 213
 <211> 1051
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(998)

<400> 213
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 Met Gln
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gaa ttc agt ttg tgg tgc gat ttt ata gaa agg gat ttt tta gaa aac 104
 Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu Glu Asn
 5 10 15

gac ttt tta aag ctc att aat aag ggg gct att tgc ggg gca acg agt 152
 Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Ala Thr Ser
 20 25 30

09095913 "062901"

aac cct agt ttg ttt tgc gaa gcg atc aca aaa agc gcg ttt tat aaa	200
Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe Tyr Lys	
35 40 45 50	
gat gaa atc gct aaa ctc aaa ggc aaa aaa gct aaa gaa att tat gaa	248
Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile Tyr Glu	
55 60 65	
act ctg gcg tta aag gat att tta caa gct tct agc gcg ttg atg cct	296
Thr Leu Ala Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu Met Pro	
70 75 80	
tta tat gaa aaa gac cct aac aat ggc tac att agc cta gaa att gac	344
Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu Ile Asp	
85 90 95	
cct ttt tta gaa gat gat gcc gct aaa agc att gat gaa gcc aag cgg	392
Pro Phe Leu Glu Asp Asp Ala Ala Lys Ser Ile Asp Glu Ala Lys Arg	
100 105 110	
ttg ttc aaa aca tta aac cgc cct aat gtg atg att aaa gtc cca gcg	440
Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val Pro Ala	
115 120 125 130	
agt gaa agc ggg att gaa gtg gtt agc gct tta act caa gcc tct att	488
Ser Glu Ser Gly Ile Glu Val Val Ser Ala Leu Thr Gln Ala Ser Ile	
135 140 145	
cct gtt aat gta act tta gtc ttt tcg cct aaa att gcc ggt gaa atc	536
Pro Val Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly Glu Ile	
150 155 160	
gct caa atc tta gcc aaa gaa gcg caa aaa aga gcg gtc att agc gtg	584
Ala Gln Ile Leu Ala Lys Glu Ala Gln Lys Arg Ala Val Ile Ser Val	
165 170 175	
ttt gtc tca cga ttt gac aaa gaa ata gac cct tta gtg cca aaa aat	632
Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro Lys Asn	
180 185 190	
ttg caa gct caa agc ggg att atc aac gct acc gag tgc tat tat caa	680
Leu Gln Ala Gln Ser Gly Ile Ile Asn Ala Thr Glu Cys Tyr Tyr Gln	
195 200 205 210	
att aat cag cat gcc aat aag cta aca agc acc ctt ttt gca tcc aca	728
Ile Asn Gln His Ala Asn Lys Leu Thr Ser Thr Leu Phe Ala Ser Thr	
215 220 225	
ggc gtt aaa tcc aat tct tta gct aaa gat tac tac att aaa gcg ctg	776
Gly Val Lys Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys Ala Leu	
230 235 240	
tgt ttt aaa aac tct atc aat aca gcc cct cta gag gct tta aac gct	824
Cys Phe Lys Asn Ser Ile Asn Thr Ala Pro Leu Glu Ala Leu Asn Ala	
245 250 255	
tat ttg ctt gac cca aac acc gag tgt caa acc cct tta aag act aca	872
Tyr Leu Leu Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys Thr Thr	

260

265

270

gaa att gaa gcg ttt aaa aaa gaa tta aaa gtg cac aac att gat tta 920
 Glu Ile Glu Ala Phe Lys Lys Glu Leu Lys Val His Asn Ile Asp Leu
 275 280 285 290

gaa aac acc gct caa aaa ctc ctt aaa gaa ggc ttg ata gcg ttc aaa 968
 Glu Asn Thr Ala Gln Lys Leu Leu Lys Glu Gly Leu Ile Ala Phe Lys
 295 300 305

caa tcc ttt gaa aag ctt tta agc agt ttt tgattttttaa gggtttttttg 1018
 Gln Ser Phe Glu Lys Leu Leu Ser Ser Phe
 310 315

gatagaataa gcccttatttt tatttttaaag gat 1051

<210> 214

<211> 316

<212> PRT

<213> Helicobacter pylori

<400> 214

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 Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
 35 40 45
 Tyr Lys Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile
 50 55 60
 Tyr Glu Thr Leu Ala Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu
 65 70 75 80
 Met Pro Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu
 85 90 95
 Ile Asp Pro Phe Leu Glu Asp Asp Ala Ala Lys Ser Ile Asp Glu Ala
 100 105 110
 Lys Arg Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val
 115 120 125
 Pro Ala Ser Glu Ser Gly Ile Glu Val Val Ser Ala Leu Thr Gln Ala
 130 135 140
 Ser Ile Pro Val Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly
 145 150 155 160
 Glu Ile Ala Gln Ile Leu Ala Lys Glu Ala Gln Lys Arg Ala Val Ile
 165 170 175
 Ser Val Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro
 180 185 190
 Lys Asn Leu Gln Ala Gln Ser Gly Ile Ile Asn Ala Thr Glu Cys Tyr
 195 200 205
 Tyr Gln Ile Asn Gln His Ala Asn Lys Leu Thr Ser Thr Leu Phe Ala
 210 215 220
 Ser Thr Gly Val Lys Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys
 225 230 235 240
 Ala Leu Cys Phe Lys Asn Ser Ile Asn Thr Ala Pro Leu Glu Ala Leu
 245 250 255
 Asn Ala Tyr Leu Leu Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys
 260 265 270
 Thr Thr Glu Ile Glu Ala Phe Lys Lys Glu Leu Lys Val His Asn Ile
 275 280 285
 Asp Leu Glu Asn Thr Ala Gln Lys Leu Leu Lys Glu Gly Leu Ile Ala

290 295 300
Phe Lys Gln Ser Phe Glu Lys Leu Leu Ser Ser Phe
305 310 315

<210> 215
<211> 1254
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (55)...(1215)

<400> 215
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Leu Asn Phe Met Thr Lys Lys Lys Asn Arg Met Gln Asp Cys Lys Met
5 10 15
gtt tgt aaa aat ttt aat cgt aag gaa tct gtt ttg ata gct caa tct 153
Val Cys Lys Asn Phe Asn Arg Lys Glu Ser Val Leu Ile Ala Gln Ser
20 25 30
tta gat att tct aaa aaa ggt tcg gta att tta ggc gct ctt ttg agt 201
Leu Asp Ile Ser Lys Lys Gly Ser Val Ile Leu Gly Ala Leu Leu Ser
35 40 45
tcg tta tgg ctg aca aac ccc tta aat gcc cat gaa aag aat ggc gcg 249
Ser Leu Trp Leu Thr Asn Pro Leu Asn Ala His Glu Lys Asn Gly Ala
50 55 60 65
ttt gtg ggg att agc ttg gaa gtg ggt agg gcc gat caa aag aca aac 297
Phe Val Gly Ile Ser Leu Glu Val Gly Arg Ala Asp Gln Lys Thr Asn
70 75 80
gct tat aaa aac ggc gag ttg ttt caa gtg cct ttt ggc gat gtt tcg 345
Ala Tyr Lys Asn Gly Glu Leu Phe Gln Val Pro Phe Gly Asp Val Ser
85 90 95
gct aat gat gat ggc aaa gtt cct gac ggg cag acc ggt ggc tgt cag 393
Ala Asn Asp Asp Gly Lys Val Pro Asp Gly Gln Thr Gly Gly Cys Gln
100 105 110
cca gct tca ggg acg cca gga acg cca ggc tac act aaa gct aac tgc 441
Pro Ala Ser Gly Thr Pro Gly Thr Pro Gly Tyr Thr Lys Ala Asn Cys
115 120 125
gtg gtc aat tgg act tcg cgc acc atg ctt agc acc aat aaa aac att 489
Val Val Asn Trp Thr Ser Arg Thr Met Leu Ser Thr Asn Lys Asn Ile
130 135 140 145
cct ggc cgt aac cag ccg atg tat ggg cta ggc gtg atg aca ggc tat 537
Pro Gly Arg Asn Gln Pro Met Tyr Gly Leu Gly Val Met Thr Gly Tyr
150 155 160
aag cat ttt atc ggt aaa aaa aga tgg ttt ggg ttg cgc tat tac ggc 585

Lys	His	Phe	Ile	Gly	Lys	Lys	Arg	Trp	Phe	Gly	Leu	Arg	Tyr	Tyr	Gly		
			165				170						175				
ttt	ttt	gat	tat	ggg	cat	acc	aat	ttc	tct	aac	tcc	aga	gcc	gct	aac	633	
Phe	Phe	Asp	Tyr	Gly	His	Thr	Asn	Phe	Ser	Asn	Ser	Arg	Ala	Ala	Asn		
			180				185						190				
gct	ata	tcg	cct	ttt	tat	ttg	agc	gat	caa	aaa	gcc	gac	atg	tat	act	681	
Ala	Ile	Ser	Pro	Phe	Tyr	Leu	Ser	Asp	Gln	Lys	Ala	Asp	Met	Tyr	Thr		
			195				200						205				
tat	ggg	ttt	ggc	aca	gac	atg	ctt	ttt	aac	att	ata	gat	aag	cct	aaa	729	
Tyr	Gly	Phe	Gly	Thr	Asp	Met	Leu	Phe	Asn	Ile	Ile	Asp	Lys	Pro	Lys		
			210				215						220				
gcc	acg	gcc	ggg	ttt	ttt	tta	ggc	gtg	aat	ttt	gcg	ggg	aac	act	tgg	777	
Ala	Thr	Ala	Gly	Phe	Phe	Leu	Gly	Val	Asn	Phe	Ala	Gly	Asn	Thr	Trp		
			230				235						240				
act	aat	aat	cgt	gtg	ggg	tat	ttt	aag	gac	ggg	tat	gtt	tat	ggc	gtc	825	
Thr	Asn	Asn	Arg	Val	Gly	Tyr	Phe	Lys	Asp	Gly	Tyr	Val	Tyr	Gly	Val		
			245				250						255				
aat	acg	gac	gct	gac	gct	tac	atg	act	aac	gct	gat	ggc	aca	atc	act	873	
Asn	Thr	Asp	Ala	Asp	Ala	Tyr	Met	Thr	Asn	Ala	Asp	Gly	Thr	Ile	Thr		
			260				265						270				
tgc	ggg	gac	acg	acg	ccg	gcg	agt	tgc	aat	gtg	ggg	att	aac	cct	aat	921	
Cys	Gly	Asp	Thr	Thr	Pro	Ala	Ser	Cys	Asn	Val	Gly	Ile	Asn	Pro	Asn		
			275				280						285				
agc	gtc	tat	acc	aca	gga	aaa	ttg	aac	gct	aag	gtg	aat	cac	acg	att	969	
Ser	Val	Tyr	Thr	Thr	Gly	Lys	Leu	Asn	Ala	Lys	Val	Asn	His	Thr	Ile		
			290				295						300				
ttc	caa	ttt	tta	gtg	aat	gtg	ggc	att	aga	act	aat	att	ttt	gaa	cac	1017	
Phe	Gln	Phe	Leu	Val	Asn	Val	Gly	Ile	Arg	Thr	Asn	Ile	Phe	Glu	His		
			310				315						320				
cat	ggc	att	gag	ttt	ggc	atc	aaa	atc	ccc	acg	ctc	cct	aac	tac	ttt	1065	
His	Gly	Ile	Glu	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Leu	Pro	Asn	Tyr	Phe		
			325				330						335				
ttc	aaa	ggg	tct	act	acc	ata	aga	gcg	aaa	aaa	caa	ggc	ccg	cta	gag	1113	
Phe	Lys	Gly	Ser	Thr	Thr	Ile	Arg	Ala	Lys	Lys	Gln	Gly	Pro	Leu	Glu		
			340				345						350				
aat	ggc	caa	cca	acc	act	atc	acc	gga	gca	gaa	acc	aat	ttc	agc	tta	1161	
Asn	Gly	Gln	Pro	Thr	Thr	Ile	Thr	Gly	Ala	Glu	Thr	Asn	Phe	Ser	Leu		
			355				360						365				
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Thr	Phe																

SECRET

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 Tyr Leu Asp Leu Ile Gly Phe Phe Lys Ser Arg Asp Phe Phe Glu Pro
 135 140 145

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gat Asp 370	gat Asp	tat Tyr	ggg Gly	gtg Val	ggc Gly 375	gtg Val	ttt Phe	tct Ser	caa Gln	tta Leu 380	gtc Val	cag Gln	cac His	agc Ser	gtt Val 385	1208
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ttt Phe 435	ctt Leu	aaa Lys	tta Leu	aaa Lys	gct Ala	aaa Lys 440	gtc Val	agg Arg	act Thr	aag Lys 445	ctt Leu 445	tta Leu	gag Glu	att Ile	gct Ala	1400
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SECRET

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Gly	Val	Lys	Val	Ala	Arg	Leu	Asp	Arg	Tyr	Ala	Ser	Glu	Lys	Asn	Lys
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Leu	Leu	Lys	Ala	Val	Glu	Leu	Gly	Gln	Val	Asp	Ala	Leu	Ile	Gly	Thr
			580					585					590		
His	Ala	Ile	Leu	Gly	Ala	Lys	Phe	Lys	Asn	Leu	Gly	Leu	Val	Val	Val
		595					600					605			
Asp	Glu	Glu	His	Lys	Phe	Gly	Val	Lys	Gln	Lys	Glu	Ala	Leu	Lys	Glu
	610					615					620				
Leu	Ser	Lys	Ser	Val	His	Phe	Leu	Ser	Met	Ser	Ala	Thr	Pro	Ile	Pro
625					630					635					640
Arg	Thr	Leu	Asn	Met	Ala	Leu	Ser	Gln	Ile	Lys	Gly	Ile	Ser	Ser	Leu
				645					650					655	
Lys	Thr	Pro	Pro	Thr	Asp	Arg	Lys	Pro	Ser	Arg	Thr	Phe	Leu	Lys	Glu
			660					665					670		
Lys	Asn	Asp	Glu	Leu	Leu	Lys	Glu	Ile	Ile	Tyr	Arg	Glu	Leu	Arg	Arg
		675					680					685			
Asn	Gly	Gln	Ile	Phe	Tyr	Ile	His	Asn	His	Ile	Ala	Ser	Ile	Leu	Lys
	690					695					700				
Val	Lys	Thr	Lys	Leu	Glu	Asp	Leu	Ile	Pro	Lys	Leu	Lys	Ile	Ala	Ile
705					710					715					720
Leu	His	Ser	Gln	Ile	Asn	Ala	Asn	Glu	Ser	Glu	Glu	Ile	Met	Leu	Glu
				725					730					735	
Phe	Ala	Lys	Gly	Asn	Tyr	Gln	Val	Leu	Leu	Cys	Thr	Ser	Ile	Val	Glu
			740					745					750		
Ser	Gly	Ile	His	Leu	Pro	Asn	Ala	Asn	Thr	Ile	Ile	Ile	Asp	Asn	Ala
		755					760						765		
Gln	Asn	Phe	Gly	Leu	Ala	Asp	Leu	His	Gln	Leu	Arg	Gly	Arg	Val	Gly
	770					775					780				
Arg	Gly	Lys	Lys	Glu	Gly	Phe	Cys	Tyr	Phe	Leu	Ile	Glu	Asp	Gln	Lys
785					790					795					800
Ser	Leu	Asn	Glu	Gln	Ala	Leu	Lys	Arg	Leu	Leu	Ala	Leu	Glu	Lys	Asn
				805					810					815	
Ser	Tyr	Leu	Gly	Ser	Gly	Glu	Ser	Val	Ala	Tyr	His	Asp	Leu	Glu	Ile
			820					825					830		
Arg	Gly	Gly	Gly	Asn	Leu	Leu	Gly	Gln	Asp	Gln	Ser	Gly	His	Ile	Lys
		835					840					845			
Asn	Ile	Gly	Tyr	Ala	Leu	Tyr	Thr	Arg	Met	Leu	Glu	Asp	Ala	Ile	Tyr

850	Glu Leu Ser Gly Gly Lys	855	Lys Arg Leu Glu Lys	860	Ser Val Glu Ile Gln
865	Leu Gly Val Ser Ala Phe	870	Leu Asn Pro Glu Leu	875	Ile Ala Ser Asp Ser
	885		890		895
Leu Arg Leu Asp	Leu Tyr Arg Arg	Leu Ser Leu Cys	Glu Asn Thr Asp		
900		905		910	
Glu Val Gly Gln Ile His	Glu Glu Ile Glu Asp	Arg Phe Gly Lys Ile			
915		920		925	
Asp Asp Leu Ser Ala Gln	Phe Leu Gln Ile Ile	Thr Leu Lys Ile Leu			
930		935		940	
Ala Asn Gln Leu Gly Ile	Ile Lys Leu Ser Asn	Phe Asn Gln Asn Ile			
945		950		955	
Thr Ile Thr Tyr Ser	Asp Glu Lys Lys Glu	Ser Leu Lys Ala Pro Ser			
965		970		975	
Lys Asp Asp Asn Asp	Ile Leu Glu Thr Leu	Leu Lys His Leu Arg Ala			
980		985		990	
Gln Ile Ser Leu Lys	Arg Arg				
995					

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 <213> Helicobacter pylori

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atc cct att gcc ttt gcc ttt gat aaa aac tac cta aaa aca ggg gct	105
Ile Pro Ile Ala Phe Ala Phe Asp Lys Asn Tyr Leu Lys Thr Gly Ala	
5 10 15 20	
gtg gct ctc tac tct tta ttg cat gcc cat cgt gca gtt gaa ggg gta	153
Val Ala Leu Tyr Ser Leu Leu His Ala His Arg Ala Val Glu Gly Val	
25 30 35	
ttt ttc agt atc tat ata ttc tat agc ggt ttg aat gaa gat gat tta	201
Phe Phe Ser Ile Tyr Ile Phe Tyr Ser Gly Leu Asn Glu Asp Asp Leu	
40 45 50	
aac agg ctc caa gaa act atc aaa cct ttc aaa cat ttt gcc gct tta	249
Asn Arg Leu Gln Glu Thr Ile Lys Pro Phe Lys His Phe Ala Ala Leu	
55 60 65	
aaa tgc caa gat att agc gcc act ctt gat tct ttg ccc acc atc acg	297
Lys Cys Gln Asp Ile Ser Ala Thr Leu Asp Ser Leu Pro Thr Ile Thr	
70 75 80	
gat agt gca tgg gtt aat cgc tat tct aga atg att ttg gtc aaa tac	345
Asp Ser Ala Trp Val Asn Arg Tyr Ser Arg Met Ile Leu Val Lys Tyr	
85 90 95 100	
ctt ctc cct agt tta ttc ccc caa tac agc aaa atg att tgg tct gat	393

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Leu	Leu	Pro	Ser	Leu	Phe	Pro	Gln	Tyr	Ser	Lys	Met	Ile	Trp	Ser	Asp	
				105					110					115		
gtg	gat	gtg	gtc	ttt	tgc	aga	gct	ttc	gct	gat	gat	ttt	atc	gct	tta	441
Val	Asp	Val	Val	Phe	Cys	Arg	Ala	Phe	Ala	Asp	Asp	Phe	Ile	Ala	Leu	
				120				125					130			
gac	aca	agc	gaa	tct	ttt	cat	ttg	agt	ggg	gtg	ata	agt	tta	gta	tca	489
Asp	Thr	Ser	Glu	Ser	Phe	His	Leu	Ser	Gly	Val	Ile	Ser	Leu	Val	Ser	
			135				140					145				
caa	tca	gtt	aca	gag	ggg	ttt	tgg	ttt	tgc	aat	ttg	gat	tac	atg	cga	537
Gln	Ser	Val	Thr	Glu	Gly	Phe	Trp	Phe	Cys	Asn	Leu	Asp	Tyr	Met	Arg	
		150					155				160					
aag	cac	tct	ttc	acc	caa	cag	gtc	tta	gaa	aaa	ttt	aaa	att	caa	gta	585
Lys	His	Ser	Phe	Thr	Gln	Gln	Val	Leu	Glu	Lys	Phe	Lys	Ile	Gln	Val	
					170					175					180	
atg	cgt	cca	tat	ttt	aaa	gaa	cct	aca	tta	ata	cac	cat	ttg	cat	gct	633
Met	Arg	Pro	Tyr	Phe	Lys	Glu	Pro	Thr	Leu	Ile	His	His	Leu	His	Ala	
				185					190					195		
tat	att	aaa	gaa	ctt	ccc	tta	cac	tat	tgc	gtt	ctg	cct	tat	tat	tat	681
Tyr	Ile	Lys	Glu	Leu	Pro	Leu	His	Tyr	Cys	Val	Leu	Pro	Tyr	Tyr	Tyr	
			200					205					210			
caa	gaa	gaa	ctt	gat	gat	ttg	aga	cat	aaa	gct	tcc	tta	ccc	att	cgg	729
Gln	Glu	Glu	Leu	Asp	Asp	Leu	Arg	His	Lys	Ala	Ser	Leu	Pro	Ile	Arg	
			215				220					225				
ttt	gaa	atc	atc	cac	caa	gac	aaa	ccc	aat	gaa	ttt	atc	cat	cgc	cag	777
Phe	Glu	Ile	Ile	His	Gln	Asp	Lys	Pro	Asn	Glu	Phe	Ile	His	Arg	Gln	
		230				235					240					
caa	atc	ccc	tat	gag	atc	tct	caa	att	caa	aac	att	ctt	tca	aac	cct	825
Gln	Ile	Pro	Tyr	Glu	Ile	Ser	Gln	Ile	Gln	Asn	Ile	Leu	Ser	Asn	Pro	
				245		250				255					260	
att	atc	atg	cac	tat	gaa	tct	gat	aaa	gat	gct	ctt	gga	atc	tac	aat	873
Ile	Ile	Met	His	Tyr	Glu	Ser	Asp	Lys	Asp	Ala	Leu	Gly	Ile	Tyr	Asn	
				265					270					275		
ggc	aaa	cct	tgg	gag	ttc	cct	ttg	ggg	aat	caa	tac	cac	ctg	tgg	tta	921
Gly	Lys	Pro	Trp	Glu	Phe	Pro	Leu	Gly	Asn	Gln	Tyr	His	Leu	Trp	Leu	
			280					285					290			
gag	atg	ctt	gca	cac	act	cca	ttt	tgg	aaa	gac	ttc	act	ctg	gaa	atg	969
Glu	Met	Leu	Ala	His	Thr	Pro	Phe	Trp	Lys	Asp	Phe	Thr	Leu	Glu	Met	
			295				300					305				
caa	aaa	aaa	cgc	ata	gaa	tac	cga	gat	att	gct	caa	aaa	atc	cat	tat	1017
Gln	Lys	Lys	Arg	Ile	Glu	Tyr	Arg	Asp	Ile	Ala	Gln	Lys	Ile	His	Tyr	
			310			315					320					
ttt	tct	caa	gat	aag	cgt	ctt	tat	gaa	gtg	agc	ata	cgc	tcc	att	aag	1065
Phe	Ser	Gln	Asp	Lys	Arg	Leu	Tyr	Glu	Val	Ser	Ile	Arg	Ser	Ile	Lys	
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 Glu Arg Trp Ser Lys Pro Ile Lys Thr Phe Phe Gln Lys Asn Phe Phe
 355 360 365
 Gln Lys Lys Phe
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 taaagagtga aagcggtttt aggagcgta gagtttcaag agaatgaata tgaagagctt 120
 aaagagcttt atgagagctt aaaaaaccaag caaaagcccc acactttgtt cattttctgt 180
 gtggattcac gagtcgtgcc taatttaatc actggcacca aaccgggcga attgtatgtg 240
 atttgcaac atg ggc aat gtg aac ccc cct aaa aca agc tat aaa gag tcc 291
 Met Gly Asn Val Asn Pro Pro Lys Thr Ser Tyr Lys Glu Ser
 1 5 10

 ctt tct acc att gcg agc att gaa tac gct atc gcg cat gtg ggc gtt 339
 Leu Ser Thr Ile Ala Ser Ile Glu Tyr Ala Ile Ala His Val Gly Val
 15 20 25 30

 caa aac tta atc att tgc ggg cat agc gat tgt ggg gct tgc ggg agc 387
 Gln Asn Leu Ile Ile Cys Gly His Ser Asp Cys Gly Ala Cys Gly Ser
 35 40 45

 gtt cat tta atc cat gat gaa acc acc aaa gct aaa acc cct tac att 435
 Val His Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile
 50 55 60

 gca aac tgg ata caa ttt tta gag cct gtt aaa gaa gag tta aaa aac 483
 Ala Asn Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn
 65 70 75

 cac ccg caa ttc agc aac cat ttc gcc aag cgt tca tgg ctt aca gag 531
 His Pro Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu
 80 85 90

 cgt ttg aat gcg cgc ttg caa ctc aac aac ctc tta agc tat gat ttc 579
 Arg Leu Asn Ala Arg Leu Gln Leu Asn Asn Leu Leu Ser Tyr Asp Phe
 95 100 105 110

 att caa gag aaa gcg agc aag aat gaa tta aaa att ttt ggt tgg cac 627
 Ile Gln Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His
 115 120 125

 tac atc ata gaa aca ggc agg att tat aat tat aat ttt gaa agc cat 675
 Tyr Ile Ile Glu Thr Gly Arg Ile Tyr Asn Tyr Asn Phe Glu Ser His
 130 135 140

 ttt ttt gag ccg att gga gaa acc att aaa caa agg aaa agt cat gaa 723
 Phe Phe Glu Pro Ile Gly Glu Thr Ile Lys Gln Arg Lys Ser His Glu
 145 150 155

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1				5					10					15	
Ser	Ser	Leu	Phe	Ala	Glu	Gly	Leu	Glu	Gly	Phe	Phe	Asn	Ala	Leu	Glu
			20					25					30		
Ala	Gln	Leu	Lys	Ser	Pro	Ile	Ala	Lys	Gly	Ile	Leu	Met	Val	Ile	Phe
		35					40					45			
Ile	Gly	Ile	Ala	Ile	Tyr	Val	Trp	Arg	Asn	Leu	Asp	Arg	Trp	Lys	Glu
	50				55						60				
Ile	Leu	Phe	Thr	Ile	Leu	Gly	Val	Val	Phe	Gly	Ile	Phe	Leu	Phe	Phe
65				70					75						80
Lys	Ala	Pro	Ser	Leu	Ala	Asn	Trp	Phe	Met	Gly	Ile	Phe			
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285 290 295 300	
tat cgc cct agc att ttt aaa gtc tcc gta gaa aat gat gaa gag ctt	1024
Tyr Arg Pro Ser Ile Phe Lys Val Ser Val Glu Asn Asp Glu Glu Leu	
305 310 315	
att gaa gtt gaa aag ggc gaa aat caa ggg gcg ttt tct tat ttt tta	1072
Ile Glu Val Glu Lys Gly Glu Asn Gln Gly Ala Phe Ser Tyr Phe Leu	
320 325 330	
ggc ggc cct act tgt tta gcg ggg gat ttt atg ggg agt ttt agc ttt	1120
Gly Gly Pro Thr Cys Leu Ala Gly Asp Phe Met Gly Ser Phe Ser Phe	
335 340 345	
gaa acg cct tta aaa agg ggc gat aaa atc gtg ttt caa gac atg ctc	1168
Glu Thr Pro Leu Lys Arg Gly Asp Lys Ile Val Phe Gln Asp Met Leu	
350 355 360	
cat tat acg att gtc aaa aac aac tcg ttt aat ggc gtg ccg ctc cca	1216
His Tyr Thr Ile Val Lys Asn Asn Ser Phe Asn Gly Val Pro Leu Pro	
365 370 375 380	
agc ctg gct aga ttg gat caa caa ggg ttt aaa atc ctt aaa aac ttt	1264
Ser Leu Ala Arg Leu Asp Gln Gln Gly Phe Lys Ile Leu Lys Asn Phe	
385 390 395	
tct tat gaa gac tat aaa aac aga aac taaagctttt gattaaggct	1311
Ser Tyr Glu Asp Tyr Lys Asn Arg Asn	
400 405	
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Ser Gly Ala Lys Val Leu Leu Ala Leu Lys Gly Tyr Ala Phe Trp Arg	
35 40 45	
Glu Phe Gly Ile Leu Arg Gln Lys Leu Asn Gly Cys Cys Ala Ser Gly	
50 55 60	
Leu Tyr Glu Ala Lys Leu Ala Phe Glu Glu Phe Gly Gly Arg Glu Ser	
65 70 75 80	
His Lys Glu Ile Cys Val Tyr Ser Pro Ala Phe Lys Glu Ala Glu Met	
85 90 95	
Ser Ala Ile Leu Pro Leu Ala Thr Ser Ile Ile Phe Asn Ser Phe Tyr	
100 105 110	
Gln Tyr Ala Thr Tyr Lys Asp Arg Ile Leu Asp Lys Asn Lys Gln Leu	
115 120 125	
Glu Asn Leu Gly Leu Ser Pro Ile Lys Met Gly Leu Arg Ile Asn Pro	
130 135 140	
Leu Tyr Ser Glu Val Thr Pro Ala Ile Tyr Asn Pro Cys Ser Lys Val	

tat aac att tcg gtt aaa aac aat ttt ccc acc cta aag agc gct aaa	263
Tyr Asn Ile Ser Val Lys Asn Asn Phe Pro Thr Leu Lys Ser Ala Lys	
35 40 45	
agg caa ggc ata gat ttt ggg gaa tgg gat aaa aat ttc aag ctt tta	311
Arg Gln Gly Ile Asp Phe Gly Glu Trp Asp Lys Asn Phe Lys Leu Leu	
50 55 60	
gaa tgg atc gca cgc tac gcc ccc tta gtc aat cca aac ggc tgc atg	359
Glu Trp Ile Ala Arg Tyr Ala Pro Leu Val Asn Pro Asn Gly Cys Met	
65 70 75	
gtt att ttt tgc tct tac agg ttt ata agc tat atc gct gat ttt tta	407
Val Ile Phe Cys Ser Tyr Arg Phe Ile Ser Tyr Ile Ala Asp Phe Leu	
80 85 90 95	
gaa gaa aac ggc ttt gtg gtc aaa gac ttt atc caa tgg gtt aaa aat	455
Glu Glu Asn Gly Phe Val Val Lys Asp Phe Ile Gln Trp Val Lys Asn	
100 105 110	
aat ccc atg cca aga aac att cac cgg cgt tat gtc caa gac acg gaa	503
Asn Pro Met Pro Arg Asn Ile His Arg Arg Tyr Val Gln Asp Thr Glu	
115 120 125	
ttt gct ctg tgg gcg gtt aaa aag aaa gcc aag tgg gtg ttt aac aaa	551
Phe Ala Leu Trp Ala Val Lys Lys Lys Ala Lys Trp Val Phe Asn Lys	
130 135 140	
ccc aaa aat gaa aaa tat tta cgg cct ttg att tta aaa agc cct gtg	599
Pro Lys Asn Glu Lys Tyr Leu Arg Pro Leu Ile Leu Lys Ser Pro Val	
145 150 155	
gta agc ggg ctt gaa aaa acc aaa cac ccc acg caa aaa agc ctg gcc	647
Val Ser Gly Leu Glu Lys Thr Lys His Pro Thr Gln Lys Ser Leu Ala	
160 165 170 175	
tta atg gaa aaa atc att tcc atc cac aca aac cct aat gac atc gtg	695
Leu Met Glu Lys Ile Ile Ser Ile His Thr Asn Pro Asn Asp Ile Val	
180 185 190	
cta gat cct ttc atg ggg agc ggc acc acc ggc tta gcg tgc aaa aat	743
Leu Asp Pro Phe Met Gly Ser Gly Thr Thr Gly Leu Ala Cys Lys Asn	
195 200 205	
tta gaa cgg aat ttt atc ggc ata gaa tca gaa aaa gaa tat ttt caa	791
Leu Glu Arg Asn Phe Ile Gly Ile Glu Ser Glu Lys Glu Tyr Phe Gln	
210 215 220	
acc gct aaa aag cgt ttg aat ctg ttt taaaaacgct atttgaatga	838
Thr Ala Lys Lys Arg Leu Asn Leu Phe	
225 230	
gattgtgtta tagttattta aaaggatatt ttga	872

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 <212> PRT
 <213> Helicobacter pylori

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 20 25 30
 Asn Ile Ser Val Lys Asn Asn Phe Pro Thr Leu Lys Ser Ala Lys Arg
 35 40 45
 Gln Gly Ile Asp Phe Gly Glu Trp Asp Lys Asn Phe Lys Leu Leu Glu
 50 55 60
 Trp Ile Ala Arg Tyr Ala Pro Leu Val Asn Pro Asn Gly Cys Met Val
 65 70 75 80
 Ile Phe Cys Ser Tyr Arg Phe Ile Ser Tyr Ile Ala Asp Phe Leu Glu
 85 90 95
 Glu Asn Gly Phe Val Val Lys Asp Phe Ile Gln Trp Val Lys Asn Asn
 100 105 110
 Pro Met Pro Arg Asn Ile His Arg Arg Tyr Val Gln Asp Thr Glu Phe
 115 120 125
 Ala Leu Trp Ala Val Lys Lys Lys Ala Lys Trp Val Phe Asn Lys Pro
 130 135 140
 Lys Asn Glu Lys Tyr Leu Arg Pro Leu Ile Leu Lys Ser Pro Val Val
 145 150 155 160
 Ser Gly Leu Glu Lys Thr Lys His Pro Thr Gln Lys Ser Leu Ala Leu
 165 170 175
 Met Glu Lys Ile Ile Ser Ile His Thr Asn Pro Asn Asp Ile Val Leu
 180 185 190
 Asp Pro Phe Met Gly Ser Gly Thr Thr Gly Leu Ala Cys Lys Asn Leu
 195 200 205
 Glu Arg Asn Phe Ile Gly Ile Glu Ser Glu Lys Glu Tyr Phe Gln Thr
 210 215 220
 Ala Lys Lys Arg Leu Asn Leu Phe
 225 230

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 Met Asn Tyr Lys Ile Leu Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser
 1 5 10 15
 gct ggg tta gag tgt tta gaa gag ttt gac gct tta ata ggg cta gat 155
 Ala Gly Leu Glu Cys Leu Glu Glu Phe Asp Ala Leu Ile Gly Leu Asp
 20 25 30
 tgc gat aaa caa gcc cta atc act ttt gaa aac aac cat aaa aac gcc 203
 Cys Asp Lys Gln Ala Leu Ile Thr Phe Glu Asn Asn His Lys Asn Ala
 35 40 45
 ata ggc gtt tgt ggg gac atc act caa acc gaa att aaa gaa aaa gtc 251
 Ile Gly Val Cys Gly Asp Ile Thr Gln Thr Glu Ile Lys Glu Lys Val
 50 55 60

atc acg cct aga gaa gcc gct agg ata caa agt ttt agc gat aat tat 1019
Ile Thr Pro Arg Glu Ala Ala Arg Ile Gln Ser Phe Ser Asp Asn Tyr
305 310 315 320

atc ttt tat ggc aat aaa acg agc gtt tgt aag caa atc ggt aac gct 1067
Ile Phe Tyr Gly Asn Lys Thr Ser Val Cys Lys Gln Ile Gly Asn Ala
325. 330 335

gtg cct cct ctt cta gcc cta gcc tta ggc aaa gcg atc tta aaa agc 1115
Val Pro Pro Leu Leu Ala Leu Ala Leu Gly Lys Ala Ile Leu Lys Ser
340 345 350

tta aga aaa tgatacaaat ttatcacgct gacgcttttg aaatcatcaa 1164
Leu Arg Lys
355

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<212> PRT
<213> Helicobacter pylori
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Ala	Gly	Leu	Glu	Cys 20	Leu	Glu	Glu	Phe 25	Asp	Ala	Leu	Ile	Gly 30	Leu	Asp
Cys	Asp	Lys 35	Gln	Ala	Leu	Ile	Thr 40	Phe	Glu	Asn	Asn	His 45	Lys	Asn	Ala
Ile	Gly 50	Val	Cys	Gly	Asp 55	Ile	Thr	Gln	Thr	Glu	Ile 60	Lys	Glu	Lys	Val
Ile 65	Lys	Leu	Ala	Lys 70	Lys	Leu	Glu	Ile	Asn 75	Met	Ile	Ile	Gly	Gly	Pro 80
Pro	Cys	Gln	Gly	Phe 85	Ser	Asn	Lys	Gly	Lys 90	Asn	Leu	Gly	Leu	Lys 95	Asp
Pro	Arg	Asn 100	Phe	Leu	Phe	Leu	Glu	Tyr 105	Ile	Glu	Ile	Val 110	Lys	Ala	Ile
Lys	Pro	Glu 115	Ile	Phe	Ile	Ile	Glu	Asn 120	Val	Lys	Asn 125	Leu	Ile	Ser	Cys
Ala	Lys 130	Gly	Tyr	Phe	Leu	Glu 135	Glu	Ile	Lys	Glu	Arg 140	Leu	Asn	Ala	Leu
Gly 145	Tyr	Gln	Leu	Ser 150	Tyr	Gln	Ile	Leu	Asn 155	Ala	Lys	Asp	Tyr	Gly 160	Val
Pro	Gln	Asn	Arg	Glu 165	Arg	Ala	Phe	Ile	Val 170	Gly	Ala	Ser	Arg	Phe 175	Ser
Phe	Asp	Phe 180	Asn	Leu	Leu	Glu	Pro	Ser 185	Gln	Ser	Val	Asn 190	Val	Gln	Asp
Ala	Ile	Ser 195	Asp	Leu	Ala	Tyr 200	Leu	Cys	Ser	Asn	Glu 205	Gly	Ala	Phe	Glu
Ser	Asp 210	Tyr	Leu	Asn 215	Pro	Ile	Gln	Ser	Ser	Tyr 220	Gln	Ala	Leu	Met	Arg
Lys 225	Asp	Ser	Pro	Lys 230	Leu	Tyr	Asn	His	Gln 235	Ala	Thr	Asn	His	Ser	Gln 240
Ala	Ala	Leu	Glu	Lys 245	Leu	Lys	Leu	Ile	Asn 250	Lys	Glu	Gln	Gly	Lys 255	Glu
Cys	Leu	Pro	Lys 260	Asn	Leu	His	Gly 265	Lys	Gln	Phe	Lys 270	Ser	Thr	Trp	

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agt Ser	ggg Gly	att Ile 150	tat Tyr	cct Pro	tta Leu	ttt Phe	gac Asp 155	aac Asn	ttt Phe	tta Leu	caa Gln	aaa Lys 160	caa Gln	gac Asp	aca Thr	537
gaa Glu	agt Ser 165	ttt Phe	aag Lys	caa Gln	cta Leu	aaa Lys 170	gat Asp	ggg Gly	ttc Phe	act Thr	cat His 175	ttt Phe	act Thr	atc Ile	aat Asn	585
aac Asn 180	aca Thr	gca Ala	atc Ile	aat Asn	aac Asn 185	gct Ala	acg Thr	gaa Glu	tgt Cys	ttt Phe 190	agg Arg	att Ile	ttt Phe	act Thr	aaa Lys 195	633
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ggg Gly	tat Tyr	ttg Leu	tcc Ser 215	aac Asn	act Thr	ata Ile	att Ile	aca Thr 220	aaa Lys	gat Asp	gag Glu	ctt Leu 225	aat Asn	tat Tyr	aat Asn	729
cgt Arg	atc Ile	aat Asn 230	tgg Trp	cga Arg	gat Asp	ata Ile	gga Gly 235	aaa Lys	gat Asp	aaa Lys	aat Asn	acc Thr 240	acc Thr	aga Arg	caa Gln	777
gaa Glu	tac Tyr 245	gat Asp	ctt Leu	ata Ile	aac Asn	tct Ser 250	aaa Lys	agg Arg	att Ile	gct Ala	aat Asn 255	tct Ser	aac Asn	tat Tyr	ctt Leu	825
att Ile 260	tca Ser	aaa Lys	gct Ala	aag Lys	aaa Lys 265	gtg Val	gtg Val	aaa Lys	cga Arg	tat Tyr 270	aat Asn	gat Asp	aga Arg	ttt Phe	aat Asn 275	873
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caa Gln	ata Ile	cac His	cat His 295	att Ile	ttt Phe	ccc Pro	atc Ile	caa Gln 300	gac Asp	ttt Phe	ccc Pro	att Ile 305	att Ile	gct Ala	aac Asn	969
tat Tyr	ata Ile	gag Glu 310	aat Asn	ctt Leu	atc Ile	gca Ala	ctc Leu 315	act Thr	cct Pro	aat Asn	caa Gln	cat His 320	ttt Phe	att Ile	tac Tyr	1017
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atc Ile 340	tgc Cys	tta Leu	tta Leu	gct Ala	aaa Lys 345	acg Thr	acc Thr	aca Thr	att Ile	ctt Leu 350	aat Asn	gac Asp	act Thr	caa Gln	ggc Gly 355	1113
gta Val	tat Tyr	gat Asp	tgg Trp	aat Asn 360	gat Asp	tat Tyr	att Ile	gtt Val 365	gtg Val	ttg Leu	aat Asn	atg Met	ggc Gly 370	ctc Leu	aaa Lys	1161

aca act atc ttt tct caa gtc aag aac gaa tgg gaa tta tta aaa gta 1209
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 Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp Pro Ser Trp
 390 395 400

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 35 40 45
 Asn Ile Gly Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr
 50 55 60
 Thr Asn Glu Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser
 65 70 75 80
 Asp Phe Ser Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys
 85 90 95
 Leu Leu Ala Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg
 100 105 110
 Asn Ile Tyr Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln
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 Arg Glu Thr Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val
 130 135 140
 Leu Met Asp Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys
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 Gln Asp Thr Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe
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 Thr Ile Asn Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile
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 Phe Thr Lys Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly
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 Thr Arg Lys Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu
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 Arg Phe Asn Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser
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 Gln Ala Thr Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile
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Ile Ala Asn Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His
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 Phe Ile Tyr Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp
 325 330 335
 Phe Gln Tyr Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp
 340 345 350
 Thr Gln Gly Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met
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 Gly Leu Lys Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu
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 Leu Lys Val Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp
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 Met Leu Phe Asp Gln Thr Leu Thr
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 tat att tct tta ttt tct ggg gca gga gtg ggg tgc tat ggg ctt tta 161
 Tyr Ile Ser Leu Phe Ser Gly Ala Gly Val Gly Cys Tyr Gly Leu Leu
 10 15 20
 gaa gag ggg ttt gaa tgc gtt gct acc aat gaa att tta gaa aaa cgc 209
 Glu Glu Gly Phe Glu Cys Val Ala Thr Asn Glu Ile Leu Glu Lys Arg
 25 30 35 40
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 Leu Asn Ile Gln Arg Ile Asn Arg Lys Cys Lys Leu Asp Glu Ser Tyr
 45 50 55
 att agt ggg gac att aaa aag cca gaa aca aaa gaa aaa att tta aag 305
 Ile Ser Gly Asp Ile Lys Lys Pro Glu Thr Lys Glu Lys Ile Leu Lys
 60 65 70
 caa att gaa ttt tat tct aaa aaa ttt ggt aat gat agg gtt gat tta 353
 Gln Ile Glu Phe Tyr Ser Lys Lys Phe Gly Asn Asp Arg Val Asp Leu
 75 80 85
 gtg gta gca acc cca cct tgt caa ggc atg agc gta gcc aat cat aag 401
 Val Val Ala Thr Pro Pro Cys Gln Gly Met Ser Val Ala Asn His Lys
 90 95 100
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 Lys Lys Asn Asp Glu Ile Lys Arg Asn Ser Leu Val Val Glu Ser Ile
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acg gat ttt tat cat agt ttt aga act tat cca aag cat atg caa gaa Thr Asp Phe Tyr His Ser Phe Arg Thr Tyr Pro Lys His Met Gln Glu 235 240 245	833
tgg att aag gat tta aaa gaa gga caa agc gcg ttt gag aat aca gaa Trp Ile Lys Asp Leu Lys Glu Gly Gln Ser Ala Phe Glu Asn Thr Glu 250 255 260	881
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gtt tct aaa aat ggc gat aaa tat aaa aga caa aaa tat cat agc gtt Val Ser Lys Asn Gly Asp Lys Tyr Lys Arg Gln Lys Tyr His Ser Val 285 290 295	977
gcc cct tgc att cat aca aga aac gac caa atg gct agc caa aac acg Ala Pro Cys Ile His Thr Arg Asn Asp Gln Met Ala Ser Gln Asn Thr 300 305 310	1025
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365				370				375								
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cac His	tta Leu	gag Glu	cct Pro	aaa Lys	gaa Glu	atc Ile	att Ile	agg Arg	ctt Leu	att Ile	gat Asp	gtg Val	cac His	cat His	tta Leu	1313
395				400				405								
tta Leu	gag Glu	cca Pro	caa Gln	aat Asn	ttg Leu	aag Lys	cga Arg	ttt Phe	att Ile	tta Leu	gaa Glu	aat Asn	caa Gln	aac Asn	aag Lys	1361
410				415				420								
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425				430				435				440				
cgc Arg	ata Ile	gaa Glu	aaa Lys	agc Ser	gcg Ala	tat Tyr	ttt Phe	aca Thr	aac Asn	cct Pro	ttt Phe	att Ile	att Ile	aat Asn	gaa Glu	1457
445				450				455								
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460				465				470								
gag Glu	cca Pro	agt Ser	gca Ala	ggg Gly	tgt Cys	ggg Gly	aat Asn	ttc Phe	tta Leu	agt Ser	gct Ala	ctt Leu	ttt Phe	aaa Lys	aaa Lys	1553
475				480				485								
tac Tyr	act Thr	tct Ser	gtt Val	aaa Lys	aaa Lys	gtt Val	tat Tyr	tta Leu	aag Lys	tgt Cys	ata Ile	gat Asp	att Ile	gat Asp	aaa Lys	1601
490				495				500								
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505				510				515				520				
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525				530				535								
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540				545				550								
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555				560				565								
ttt Phe	tta Leu	gaa Glu	aag Lys	tct Ser	tta Leu	aaa Lys	cta Leu	gcc Ala	aac Asn	ttt Phe	aca Thr	gcg Ala	atg Met	gtt Val	atg Met	1841
570				575				580								
cct Gly	aaa Lys	aac Glu	ctt Leu	tta Leu	aac Glu	act Tyr	aaa Lys	gag Glu	tat Tyr	gca Ala	gaa Glu	act Tyr	aga Tyr	act Tyr	aag Tyr	1889

Pro Lys Asn Leu Leu Asn Thr Lys Glu Tyr Ala Glu Thr Arg Thr Lys	
585 590 595 600	
ctt gaa aaa aag gga gta gga gcg att tta gac ttt ggc gag ctt ggt	1937
Leu Glu Lys Lys Gly Val Gly Ala Ile Leu Asp Phe Gly Glu Leu Gly	
605 610 615	
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Phe Lys Gly Val Leu Val Glu Thr Ile Ala Ile Val Thr Gln Lys Ser	
620 625 630	
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Lys Glu Val Leu Ala Arg Ser Leu Pro Leu Asn Leu Ser Ile Lys Gln	
635 640 645	
aag cca agc tat att ttt gac aaa caa ttg ccc tat tgg gtt atc tat	2081
Lys Pro Ser Tyr Ile Phe Asp Lys Gln Leu Pro Tyr Trp Val Ile Tyr	
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Phe Glu Val Phe Arg Asp Arg Gln Ile Thr Asn Ser Val Leu Val Lys	
685 690 695	
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Asn Gly Ile Arg Val Ile Lys Ser Arg Asn Ile Asp Glu Asn Gly Lys	
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Ile Ile Ser Ile Glu Asn Tyr Asp Ser Tyr Ile Gln Lys Glu Val Leu	
715 720 725	
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Ser Pro Phe Lys Ile Ala Ser Phe Leu Asp Arg Asp Asp Val Tyr Leu	
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Tyr Val Val Asn Gly Ser Val Ala Ile Leu Ile Pro Lys Asn Pro Ile	
765 770 775	
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Ser Leu Ser Lys Lys Gln Cys Asp Tyr Ile Ser Ser Val Glu Phe Arg	
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Asp Phe Tyr Lys Ile Ala Arg Asn Tyr Gln Thr Arg Thr Leu Asn Ile	
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Asp Ser Met Ser Cys Phe Trp Phe Gly Ile Leu Arg Ser Ser Leu	
810 815 820	

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Phe	Leu	Ser	Ala	Leu	Phe	Lys	Lys	Tyr	Thr	Ser	Val	Lys	Lys	Val	Tyr	
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Arg	Leu	Thr	His	Leu	Ala	Gly	Ile	Phe	Leu	Glu	Lys	Ser	Leu	Lys	Leu	
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Ala	Asn	Phe	Thr	Ala	Met	Val	Met	Pro	Lys	Asn	Leu	Leu	Asn	Thr	Lys	
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Glu	Tyr	Ala	Glu	Thr	Arg	Thr	Lys	Leu	Glu	Lys	Lys	Gly	Val	Gly	Ala	
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Ile	Ala	Ile	Val	Thr	Gln	Lys	Ser	Lys	Glu	Val	Leu	Ala	Arg	Ser	Leu	
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Pro	Leu	Asn	Leu	Ser	Ile	Lys	Gln	Lys	Pro	Ser	Tyr	Ile	Phe	Asp	Lys	
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Gln	Leu	Pro	Tyr	Trp	Val	Ile	Tyr	Arg	Asn	Ala	Phe	Phe	Asp	Lys	Val	
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Phe	His	Ser	Met	Gln	Phe	Gly	Leu	Phe	Glu	Val	Phe	Arg	Asp	Arg	Gln	
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SECRET

SECRET

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SECRET

gta Val	acg Thr 675	ggc Gly	tat Tyr	aag Lys	ctt Leu	tgt Cys 680	gag Glu	tgc Cys	ttt Phe	tgg Trp	gat Asp 685	gcg Ala	ggc Gly	gtg Val	cct Pro	2120
aga Arg 690	gat Asp	gcg Ala	ctc Leu	att Ile	tac Tyr 695	ttg Leu	ccc Pro	tct Ser	aaa Lys	ggg Gly 700	agc Ser	gat Asp	att Ile	agc Ser	gaa Glu 705	2168
cat His	ctt Leu	tta Leu	aga Arg	gat Asp 710	gaa Glu	agc Ser	atc Ile	cag Gln	ttt Phe 715	gcc Ala	att Ile	tta Leu	acc Thr	ggg Gly 720	ggc Gly	2216
gaa Glu	gac Asp	acc Thr	gct Ala 725	tat Tyr	aaa Lys	atg Met	tta Leu	aaa Lys 730	gct Ala	aac Asn	ccc Pro	act Thr	tta Leu 735	gcc Ala	ttg Leu	2264
agc Ser	gct Ala 740	gaa Glu	aca Thr	ggc Gly	ggg Gly	aaa Lys	aac Asn 745	gcc Ala	acc Thr	att Ile	gtg Val	agc Ser 750	aaa Lys	atg Met	gca Ala	2312
gac Asp	aga Arg 755	gac Asp	cag Gln	gcg Ala	att Ile	aag Lys 760	aat Asn	gtt Val	atc Ile	cat His	tca Ser 765	gct Ala	ttt Phe	agc Ser	aat Asn	2360
tcg Ser 770	ggg Gly	caa Gln	aaa Lys	tgc Cys	tcc Ser 775	gcc Ala	act Thr	tcg Ser	ctt Leu	tta Leu 780	gta Val	tta Leu	gaa Glu	aaa Lys	gaa Glu 785	2408
gtc Val	tat Tyr	gaa Glu	gat Asp	gag Glu 790	aac Asn	ttt Phe	aaa Lys	aag Lys	act Thr 795	cta Leu	ata Ile	gat Asp	gcg Ala	act Thr 800	cta Leu	2456
agc Ser	ctt Leu	agc Ser	gtg Val 805	ggc Gly	gat Asp	cct Pro	ttt Phe	gat Asp 810	ttc Phe	aaa Lys	aac Asn	aaa Lys	atc Ile	ggc Gly	gct Ala	2504
cta Leu	gcg Ala 820	gac Asp	aag Lys	cct Pro	aat Asn	gaa Glu	aag Lys 825	gtc Val	atc Ile	aaa Lys	gcc Ala	ata Ile	gat Asp	gaa Glu	tta Leu	2552
aaa Lys	agc Ser 835	tat Tyr	gaa Glu	aat Asn	tac Tyr	gaa Glu 840	atc Ile	ccg Pro	gta Val	agc Ser	ttt Phe 845	gtc Val	aat Asn	gat Asp	aac Asn	2600
ccc Pro 850	tat Tyr	ttg Leu	atg Met	aag Lys	cca Pro	agc Ser 855	atc Ile	aaa Lys	tac Tyr	ggc Gly 860	act Thr	aaa Lys	aaa Lys	ggc Gly	gat Asp 865	2648
ttc Phe	acg Thr	cac His	caa Gln	act Thr 870	gag Glu	ctt Leu	ttt Phe	acg Thr	ccc Pro 875	att Ile	tta Leu	tcc Ser	gtg Val	atg Met	gaa Glu	2696
gca Ala	aaa Lys	gat Asp	tta Leu 885	gac Asp	gaa Glu	gcg Ala	ata Ile	gaa Glu 890	ata Ile	gcc Ala	aat Asn	tct Ser	acc Thr 895	ggg Gly	tac Tyr	2744
ggg Gly	ctg Leu	act Thr 900	agc Ser	gcg Ala	tta Leu	gag Glu	tcg Ser 905	ttg Leu	gac Asp	gaa Glu	agg Arg	gag Glu 910	tgg Trp	gaa Glu	tat Tyr	2792

1140

1145

1150

gag cga tcg gtt agc atc tct tat cac cgt tat ggg aat tta ggc tca 3560
 Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly Ser
 1155 1160 1165

agg gtt tta agg caa ccc act tgc cac aaa tca tgc tgt gct gaa aaa 3608
 Arg Val Leu Arg Gln Pro Thr Cys His Lys Ser Cys Cys Ala Glu Lys
 170 1175 1180 1185

taaatattgt attaaataag gagatcaaaa tgggacatgt tgttttaagt acccctat 3666

<210> 246

<211> 1185

<212> PRT

<213> Helicobacter pylori

<400> 246

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 1 5 10 15
 Asp Ser Ile Ser Asn His Leu Ser Asp Gln Glu Lys Ala Phe His Ser
 20 25 30
 Lys Met Gln Lys Leu Leu Asn Asn Pro Glu Asn Lys Val Met Leu Ile
 35 40 45
 Glu Leu Met Asp Arg Ser Phe Arg Cys Leu Asp Asn Lys Ala Arg Phe
 50 55 60
 Glu Met Ile Glu His Val Leu Asp Lys Tyr Lys Ser Arg Glu Ile Phe
 65 70 75 80
 Ser Pro Phe Glu Lys Val Leu Leu Met Gly Phe Leu Ser Phe Gly Lys
 85 90 95
 Met Leu Pro Asp Met Ser Val Pro Phe Phe Val Asn Lys Ile Arg Ser
 100 105 110
 Asp Thr Lys Ala Met Val Leu Asp Gln Glu Glu Ser Gln Leu Lys Glu
 115 120 125
 Arg Ile Leu Lys Arg Lys Asn Glu Lys Ile Ile Leu Asn Val Asn Phe
 130 135 140
 Ile Gly Glu Glu Val Leu Gly Glu Glu Glu Ala Asn Ala Arg Phe Glu
 145 150 155 160
 Lys Tyr Ser Gln Ala Leu Lys Ser Asn Tyr Ile Gln Tyr Ile Ser Ile
 165 170 175
 Lys Ile Thr Thr Ile Phe Ser Gln Ile Asn Ile Leu Asp Phe Glu Tyr
 180 185 190
 Ser Lys Lys Glu Ile Val Lys Arg Leu Asp Ala Leu Tyr Ala Leu Ala
 195 200 205
 Leu Glu Glu Glu Lys Lys Gln Gly Met Pro Lys Phe Ile Asn Leu Asp
 210 215 220
 Met Glu Glu Phe Arg Asp Leu Glu Leu Thr Val Glu Ser Phe Met Glu
 225 230 235 240
 Ser Ile Ala Lys Phe Asp Leu Asn Ala Gly Ile Val Leu Gln Ala Tyr
 245 250 255
 Ile Pro Asp Ser Tyr Glu Tyr Leu Lys Lys Leu His Ala Phe Ser Lys
 260 265 270
 Glu Arg Val Leu Lys Gly Leu Lys Pro Ile Lys Ile Arg Phe Val Lys
 275 280 285
 Gly Ala Asn Met Glu Ser Glu Glu Thr Ile Ala Ser Val Lys Asp Trp
 290 295 300
 Ala Leu Pro Thr Phe Ser Asn Lys Gln Asp Thr Asp Ser Asn Tyr Asn
 305 310 315 320
 Lys Met Leu Asp Phe Val Leu Glu Gly Asp Asn Tyr Lys Tyr Ile His

0965513.052901

Ile	Gly	Ala	Ala	325	Ser	His	Asn	Ile	Phe	330	Glu	Ile	Ala	Tyr	Val	335	Tyr	Thr
Arg	Ile	His	Ala	340	Ile	Asn	Asp	Pro	Val	345	Val	Leu	Glu	His	Phe	350	Ser	Phe
Glu	Met	Leu	Glu	355	Gly	Met	Ser	Leu	Gln	360	Ala	Ser	Gln	Glu	Leu	365	Lys	Glu
Met	His	Lys	Leu	370	Ile	Leu	Tyr	Ala	Pro	375	Val	Cys	Asp	Glu	Ala	380	His	Phe
385	Asn	Asn	Ala	405	Ile	Ala	Tyr	Leu	Val	390	Arg	Arg	Leu	Asp	Glu	400	Asn	Thr
Ser	Asp	Asn	Phe	420	Met	Lys	Ala	Phe	Phe	410	Asn	Leu	Lys	Val	Gly	415	Thr	Ser
Glu	Trp	Lys	Asp	435	Gln	Glu	Gln	Arg	Phe	425	Leu	Asn	Ser	Leu	Lys	430	Gly	Ile
Ala	Thr	Leu	Asp	450	Asn	Ala	Thr	His	Arg	440	Thr	Gln	Asp	Arg	Asn	445	Ala	Lys
Gln	Ser	Gly	His	465	Thr	Thr	Tyr	Pro	Asn	455	His	Ser	Phe	Lys	Asn	460	Glu	Ser
Asp	Thr	Asp	Phe	485	Ile	Leu	Lys	Ala	Asn	470	Arg	Glu	Trp	Ala	Lys	475	Lys	Val
Arg	Glu	Lys	Met	500	Arg	Asn	Ala	Pro	Ile	490	Leu	Glu	Leu	Tyr	Pro	495	Glu	Met
Asp	Gly	Arg	Phe	515	Glu	Asp	Pro	Asn	Leu	505	Thr	Pro	Leu	Glu	Val	510	Phe	Asp
Arg	Ile	His	His	530	Lys	Lys	Ile	Ala	Ser	520	Val	His	Leu	Ala	Asp	525	Lys	Glu
Ala	Ile	Leu	Lys	545	Ala	Leu	Glu	Val	Ala	535	Lys	Ser	Asp	Lys	Ser	540	Arg	Phe
Ser	Gln	Lys	Ser	565	Phe	Thr	Glu	Ile	His	550	Ala	Leu	Met	Ser	Gln	555	Thr	Ala
Gln	Leu	Phe	Arg	580	Glu	Arg	Arg	Gly	Asp	570	Leu	Ile	Gly	Ile	Ser	575	Ala	Leu
Glu	Val	Gly	Lys	595	Thr	Phe	Ala	Glu	Thr	585	Asp	Ala	Glu	Val	Ser	590	Glu	Ala
Ile	Asp	Phe	Leu	610	Glu	Phe	Tyr	Pro	Tyr	600	Ser	Leu	Arg	Val	Leu	605	Gln	Glu
Gln	Asn	Thr	Lys	625	Thr	Gln	Phe	Thr	Pro	615	Lys	Gly	Val	Gly	Val	620	Val	Ile
Ala	Pro	Trp	Asn	645	Phe	Pro	Val	Gly	Ile	630	Ser	Val	Gly	Thr	Ile	635	Ala	Ala
Pro	Leu	Ala	Thr	660	Gly	Asn	Arg	Val	Ile	645	Tyr	Lys	Pro	Ser	Ser	650	Leu	Ser
Ser	Val	Thr	Gly	675	Tyr	Lys	Leu	Cys	Glu	660	Cys	Phe	Trp	Asp	Ala	665	Gly	Val
Pro	Arg	Asp	Ala	690	Leu	Ile	Tyr	Leu	Pro	680	Ser	Lys	Gly	Ser	Asp	685	Ile	Ser
Glu	His	Leu	Leu	705	Arg	Asp	Glu	Ser	Ile	695	Gln	Phe	Ala	Ile	Leu	700	Thr	Gly
Gly	Glu	Asp	Thr	725	Ala	Tyr	Lys	Met	Leu	710	Lys	Ala	Asn	Pro	Thr	715	Leu	Ala
Leu	Ser	Ala	Glu	740	Thr	Gly	Gly	Lys	Asn	725	Ala	Thr	Ile	Val	Ser	730	Lys	Met
Ala	Asp	Arg	Asp	755	Gln	Ala	Ile	Lys	Asn	740	Val	Ile	His	Ser	Ala	745	Phe	Ser
Asn	Ser	Gly	Gln	770	Lys	Cys	Ser	Ala	Thr	755	Ser	Leu	Leu	Val	Leu	760	Glu	Lys
Glu	Val	Tyr	Glu	785	Asp	Glu	Asn	Phe	Lys	775	Lys	Thr	Leu	Ile	Asp	780	Ala	Thr
										790						795		800

05895913 "062901

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Leu Ser Leu Ser Val Gly Asp Pro Phe Asp Phe Lys Asn Lys Ile Gly
      805      810      815
Ala Leu Ala Asp Lys Pro Asn Glu Lys Val Ile Lys Ala Ile Asp Glu
      820      825      830
Leu Lys Ser Tyr Glu Asn Tyr Glu Ile Pro Val Ser Phe Val Asn Asp
      835      840      845
Asn Pro Tyr Leu Met Lys Pro Ser Ile Lys Tyr Gly Thr Lys Lys Gly
      850      855      860
Asp Phe Thr His Gln Thr Glu Leu Phe Thr Pro Ile Leu Ser Val Met
      865      870      875      880
Glu Ala Lys Asp Leu Asp Glu Ala Ile Glu Ile Ala Asn Ser Thr Gly
      885      890      895
Tyr Gly Leu Thr Ser Ala Leu Glu Ser Leu Asp Glu Arg Glu Trp Glu
      900      905      910
Tyr Tyr Leu Glu Arg Ile Glu Ala Gly Asn Ile Tyr Ile Asn Lys Pro
      915      920      925
Thr Thr Gly Ala Ile Val Leu Arg Gln Pro Phe Gly Gly Val Lys Lys
      930      935      940
Ser Ala Val Gly Phe Gly Arg Lys Val Gly Ile Phe Asn Tyr Ile Thr
      945      950      955      960
Gln Phe Val Asn Ile Cys Gln Glu Glu Glu Asp Glu Asn Ala Leu Lys
      965      970      975
Asn Pro Leu Ser Glu Ala Leu Glu Asn Leu Thr Gln Lys Gly Tyr Asp
      980      985      990
Glu His Thr His Glu Leu Lys Arg Ala Ile Phe Met Ala Lys Ser Tyr
      995      1000      1005
Ala Tyr His Tyr Lys His Glu Phe Ser Gln Thr Lys Asp Tyr Val Lys
      1010      1015      1020
Ile Arg Gly Glu Asp Asn Leu Phe Ser Tyr Thr Lys Val Lys Ser Val
      1025      1030      1035      104
Gly Tyr Arg Ile Thr Glu Lys Asp Thr Leu Ser Asp Met Leu Gly Val
      1045      1050      1055
Ala Leu Ala Cys Leu Ile Ser Gln Ile Pro Leu Thr Leu Ser Ile Glu
      1060      1065      1070
Asn Glu Arg Thr Asn Lys Asp Leu Thr Phe Phe Leu Glu Cys Leu Lys
      1075      1080      1085
Ala Leu Gln Ala Ser Ala Pro Ile Val Tyr Glu Ser Leu Gln Lys Phe
      1090      1095      1100
Ser Glu Lys Leu Asn Thr Phe Asn Arg Val Arg Tyr Leu Lys Ser Asp
      1105      1110      1115      112
Leu Asp Leu Leu His Glu Gln Ala Ser Ala Leu Gly Met Val Leu Ala
      1125      1130      1135
Thr Ala Lys Pro Cys Leu Asn Gly Arg Phe Glu Leu Leu Tyr Tyr His
      1140      1145      1150
Leu Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly
      1155      1160      1165
Ser Arg Val Leu Arg Gln Pro Thr Cys His Lys Ser Cys Cys Ala Glu
      1170      1175      1180
Lys
1185

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<210> 247
<211> 810
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (107)...(673)

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09895913-062901

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<400> 247
agcatgaaga agtggatgtg aaggtgtgca gtatagattc acaaagcatt aaagtggggc 60
tgtttaaaga taaccaatta atctatgaaa gcgaggcaga aaaatt atg atg act 115
                                   Met Met Thr
                                   1

aag aac gcg tat gcg ttt gtt gtg att gaa gaa agc gtt atg gtg ttt 163
Lys Asn Ala Tyr Ala Phe Val Val Ile Glu Glu Ser Val Met Val Phe
    5                      10                      15

aaa cgc acc aaa gat gag ggg tta atg cct atc ttt gaa ggc ttt gtg 211
Lys Arg Thr Lys Asp Glu Gly Leu Met Pro Ile Phe Glu Gly Phe Val
    20                      25                      30                      35

cct tta aaa gag ggc ttt ttg aaa agt ttt aaa gag cgt tgc aat ttg 259
Pro Leu Lys Glu Gly Phe Leu Lys Ser Phe Lys Glu Arg Cys Asn Leu
                      40                      45                      50

gaa ttt tta gaa aat tta gac ctt ttg ttt ttg tat gac aaa cca tcc 307
Glu Phe Leu Glu Asn Leu Asp Leu Leu Phe Leu Tyr Asp Lys Pro Ser
                      55                      60                      65

gca cac gag atc ttt tcc ttg tgc aag gag ctg aaa aat tcc atc tgg 355
Ala His Glu Ile Phe Ser Leu Cys Lys Glu Leu Lys Asn Ser Ile Trp
    70                      75                      80

gac agg aag ctt gtg gta gcg cta gtg gag gct tta gag ggg ttt aag 403
Asp Arg Lys Leu Val Val Ala Leu Val Glu Ala Leu Glu Gly Phe Lys
    85                      90                      95

gat tgg aat ttg tgc ctt aaa ata gaa gac aag cgt tct aac agc ttg 451
Asp Trp Asn Leu Ser Leu Lys Ile Glu Asp Lys Arg Ser Asn Ser Leu
    100                      105                      110                      115

ggt aat ggc acc aaa aaa ttg ctc acc aac gct gat tta ggg agc gac 499
Gly Asn Gly Thr Lys Lys Leu Leu Thr Asn Ala Asp Leu Gly Ser Asp
                      120                      125                      130

tat aaa aca atc gtg ata gac agc atg aaa aca tac cac caa agc cag 547
Tyr Lys Thr Ile Val Ile Asp Ser Met Lys Thr Tyr His Gln Ser Gln
                      135                      140                      145

caa gaa aaa tat aaa aga gaa aga ggc gaa acg cta gag gtt cgc ccc 595
Gln Glu Lys Tyr Lys Arg Glu Arg Gly Glu Thr Leu Glu Val Arg Pro
    150                      155                      160

aca aca ccc cct agc tat ggg ggt gga agc att aga atc agc ggc gat 643
Thr Thr Pro Pro Ser Tyr Gly Gly Gly Ser Ile Arg Ile Ser Gly Asp
    165                      170                      175

aaa aag cct gat ttt gat gaa gaa aat ttt taaaagaaag gacaaccgat 693
Lys Lys Pro Asp Phe Asp Glu Glu Asn Phe
    180                      185

gagcagagtg caaatggata ccgaagaggt caggggaattt gtagggcatt tagaacgctt 753
taaagagttta ctaagagagg aagtgaacag cttgagtaat catttccata atttaga 810

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<210> 248
<211> 189

<212> PRT
<213> Helicobacter pylori

<400> 248
Met Met Thr Lys Asn Ala Tyr Ala Phe Val Val Ile Glu Glu Ser Val
1 5 10 15
Met Val Phe Lys Arg Thr Lys Asp Glu Gly Leu Met Pro Ile Phe Glu
20 25 30
Gly Phe Val Pro Leu Lys Glu Gly Phe Leu Lys Ser Phe Lys Glu Arg
35 40 45
Cys Asn Leu Glu Phe Leu Glu Asn Leu Asp Leu Leu Phe Leu Tyr Asp
50 55 60
Lys Pro Ser Ala His Glu Ile Phe Ser Leu Cys Lys Glu Leu Lys Asn
65 70 75 80
Ser Ile Trp Asp Arg Lys Leu Val Val Ala Leu Val Glu Ala Leu Glu
85 90 95
Gly Phe Lys Asp Trp Asn Leu Ser Leu Lys Ile Glu Asp Lys Arg Ser
100 105 110
Asn Ser Leu Gly Asn Gly Thr Lys Lys Leu Leu Thr Asn Ala Asp Leu
115 120 125
Gly Ser Asp Tyr Lys Thr Ile Val Ile Asp Ser Met Lys Thr Tyr His
130 135 140
Gln Ser Gln Gln Glu Lys Tyr Lys Arg Glu Arg Gly Glu Thr Leu Glu
145 150 155 160
Val Arg Pro Thr Thr Pro Pro Ser Tyr Gly Gly Gly Ser Ile Arg Ile
165 170 175
Ser Gly Asp Lys Lys Pro Asp Phe Asp Glu Glu Asn Phe
180 185

<210> 249
<211> 940
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (58)...(852)

<400> 249
agaaggctta gacgatgtga tcgcttggat caagcgcaac gctttattgg aagattg atg 60
Met
1

aac act tac gct caa gaa tcc aag ctc agg tta aaa acc aaa ata ggg 108
Asn Thr Tyr Ala Gln Glu Ser Lys Leu Arg Leu Lys Thr Lys Ile Gly
5 10 15

gct gat ggg cgg tgc gtg att gaa gac aat ttt ttc acg ccc ccc ttt 156
Ala Asp Gly Arg Cys Val Ile Glu Asp Asn Phe Phe Thr Pro Pro Phe
20 25 30

aag ctc atg gcg ccc ttt tac cct aaa gac gat tta gcg gaa atc atg 204
Lys Leu Met Ala Pro Phe Tyr Pro Lys Asp Asp Leu Ala Glu Ile Met
35 40 45

ctt tta gcg gta agc cct ggc atg atg agg ggc gat gcg caa gat gtg 252
Leu Leu Ala Val Ser Pro Gly Met Met Arg Gly Asp Ala Gln Asp Val
50 55 60 65

caa	tta	aac	atc	ggg	cca	aat	tgc	aag	tta	agg	atc	act	tcg	caa	tcc		300
Gln	Leu	Asn	Ile	Gly 70	Pro	Asn	Cys	Lys	Leu	Arg	Ile	Thr	Ser	Gln	Ser		
75														80			
ttt	gaa	aaa	atc	cat	aac	act	gaa	gat	ggg	ttt	gcc	agc	aga	gac	atg		348
Phe	Glu	Lys	Ile	His	Asn	Thr	Glu	Asp	Gly	Phe	Ala	Ser	Arg	Asp	Met		
85								90					95				
cat	att	gtt	gtg	ggg	gaa	aac	gct	ttt	tta	gat	ttt	gcg	cct	ttc	ccg		396
His	Ile	Val	Val	Gly	Glu	Asn	Ala	Phe	Leu	Asp	Phe	Ala	Pro	Phe	Pro		
100							105					110					
tta	atc	ccc	ttt	gaa	aac	gcg	cat	ttt	aag	ggc	aac	acc	acg	att	tct		444
Leu	Ile	Pro	Phe	Glu	Asn	Ala	His	Phe	Lys	Gly	Asn	Thr	Thr	Ile	Ser		
115						120					125						
ttg	cgc	tct	agc	tct	caa	ttg	ctc	tat	agt	gaa	atc	att	gtc	gca	ggg		492
Leu	Arg	Ser	Ser	Ser	Gln	Leu	Leu	Tyr	Ser	Glu	Ile	Ile	Val	Ala	Gly		
130					135					140					145		
cga	gtg	gcg	cgc	aat	gag	ttg	ttt	aaa	ttc	aac	cgc	ttg	cac	acc	aaa		540
Arg	Val	Ala	Arg	Asn	Glu	Leu	Phe	Lys	Phe	Asn	Arg	Leu	His	Thr	Lys		
				150					155					160			
atc	tct	att	tta	caa	gat	gag	aaa	ccc	atc	tat	tat	gac	aac	acg	att		588
Ile	Ser	Ile	Leu	Gln	Asp	Glu	Lys	Pro	Ile	Tyr	Tyr	Asp	Asn	Thr	Ile		
			165					170					175				
tta	gat	ccc	aaa	acc	acc	gac	tta	aat	aac	atg	tgc	atg	ttt	gat	ggc		636
Leu	Asp	Pro	Lys	Thr	Thr	Asp	Leu	Asn	Asn	Met	Cys	Met	Phe	Asp	Gly		
		180					185					190					
tat	acg	cat	tat	ttg	aat	ttg	gtg	ctt	gtc	aat	tgc	ccc	ata	gag	ctc		684
Tyr	Thr	His	Tyr	Leu	Asn	Leu	Val	Leu	Val	Asn	Cys	Pro	Ile	Glu	Leu		
	195					200					205						
tct	ggg	gtg	cga	gaa	tgc	att	gaa	gaa	agc	gaa	ggg	gtg	gat	ggg	gca		732
Ser	Gly	Val	Arg	Glu	Cys	Ile	Glu	Glu	Ser	Glu	Gly	Val	Asp	Gly	Ala		
210					215					220					225		
gtg	agt	gaa	acc	gct	agt	tct	cat	tta	tgc	gtg	aaa	gct	tta	gcg	aaa		780
Val	Ser	Glu	Thr	Ala	Ser	Ser	His	Leu	Cys	Val	Lys	Ala	Leu	Ala	Lys		
				230					235					240			
ggc	tca	gaa	ccc	tta	ttg	cat	tta	aga	gaa	aaa	atc	gct	cgc	ttg	gtt		828
Gly	Ser	Glu	Pro	Leu	Leu	His	Leu	Arg	Glu	Lys	Ile	Ala	Arg	Leu	Val		
			245					250					255				
acg	caa	acc	acc	acg	caa	aag	gtt	tgaaagcact				tcaaaaaagat			taaagtcctt		882
Thr	Gln	Thr	Thr	Thr	Gln	Lys	Val	265									

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<210> 250
<211> 265
<212> PRT
<213> Helicobacter pylori
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05895913.052901

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<400> 250
Met Asn Thr Tyr Ala Gln Glu Ser Lys Leu Arg Leu Lys Thr Lys Ile
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Gly Ala Asp Gly Arg Cys Val Ile Glu Asp Asn Phe Phe Thr Pro Pro
 20          25          30
Phe Lys Leu Met Ala Pro Phe Tyr Pro Lys Asp Asp Leu Ala Glu Ile
 35          40          45
Met Leu Leu Ala Val Ser Pro Gly Met Met Arg Gly Asp Ala Gln Asp
 50          55          60
Val Gln Leu Asn Ile Gly Pro Asn Cys Lys Leu Arg Ile Thr Ser Gln
 65          70          75          80
Ser Phe Glu Lys Ile His Asn Thr Glu Asp Gly Phe Ala Ser Arg Asp
 85          90          95
Met His Ile Val Val Gly Glu Asn Ala Phe Leu Asp Phe Ala Pro Phe
100          105          110
Pro Leu Ile Pro Phe Glu Asn Ala His Phe Lys Gly Asn Thr Thr Ile
115          120          125
Ser Leu Arg Ser Ser Ser Gln Leu Leu Tyr Ser Glu Ile Ile Val Ala
130          135          140
Gly Arg Val Ala Arg Asn Glu Leu Phe Lys Phe Asn Arg Leu His Thr
145          150          155          160
Lys Ile Ser Ile Leu Gln Asp Glu Lys Pro Ile Tyr Tyr Asp Asn Thr
165          170          175
Ile Leu Asp Pro Lys Thr Thr Asp Leu Asn Asn Met Cys Met Phe Asp
180          185          190
Gly Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn Cys Pro Ile Glu
195          200          205
Leu Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu Gly Val Asp Gly
210          215          220
Ala Val Ser Glu Thr Ala Ser Ser His Leu Cys Val Lys Ala Leu Ala
225          230          235          240
Lys Gly Ser Glu Pro Leu Leu His Leu Arg Glu Lys Ile Ala Arg Leu
245          250          255
Val Thr Gln Thr Thr Thr Gln Lys Val
260          265

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<210> 251
<211> 1815
<212> DNA
<213> Helicobacter pylori

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<220>
<221> CDS
<222> (51)...(1757)

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<400> 251
atggcgctaa aagcgatgac aactatgtaa aaacaattaa ggagtaagaa atg aaa      56
                                         Met Lys
                                         1

aag att agc aga aaa gaa tat gtt tct atg tat ggc cct act aca ggc      104
Lys Ile Ser Arg Lys Glu Tyr Val Ser Met Tyr Gly Pro Thr Thr Gly
 5          10          15

gat aaa gtg aga ttg ggc gat aca gac ttg atc gct gaa gta gaa cat      152
Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Ile Ala Glu Val Glu His
 20          25          30

gac tac acc att tat ggc gaa gag ctt aaa ttc ggt ggc ggt aaa acc      200

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Asp 35	Tyr	Thr	Ile	Tyr	Gly 40	Glu	Glu	Leu	Lys	Phe 45	Gly	Gly	Gly	Lys	Thr 50	
ctg Leu	aga Arg	gaa Glu	ggc Gly	atg Met 55	agc Ser	caa Gln	tcc Ser	aac Asn	aac Asn 60	cct Pro	agc Ser	aaa Lys	gaa Glu	gaa Glu 65	ttg Leu	248
gat Asp	cta Leu	atc Ile	atc Ile 70	act Thr	aac Asn	gct Ala	tta Leu	atc Ile 75	gtg Val	gat Asp	tac Tyr	acc Thr	ggg Gly 80	att Ile	tat Tyr	296
aaa Lys	gcg Ala	gat Asp 85	att Ile	ggg Gly	att Ile	aaa Lys	gat Asp 90	ggc Gly	aaa Lys	atc Ile	gct Ala	ggc Gly 95	att Ile	ggg Gly	aaa Lys	344
ggc Gly 100	ggg Gly	aac Asn	aaa Lys	gac Asp	atg Met	caa Gln 105	gat Asp	ggc Gly	gtt Val	aaa Lys	aac Asn 110	aat Asn	ctt Leu	agc Ser	gta Val	392
ggg Gly 115	cct Pro	gct Ala	act Thr	gaa Glu	gcc Ala 120	tta Leu	gcc Ala	ggg Gly	gaa Glu	ggg Gly 125	ttg Leu	atc Ile	gta Val	act Thr	gct Ala 130	440
ggg Gly	ggg Gly	att Ile	gac Asp	aca Thr 135	cac His	atc Ile	cac His	ttc Phe	att Ile 140	tca Ser	ccc Pro	caa Gln	caa Gln	atc Ile 145	cct Pro	488
aca Thr	gct Ala	ttt Phe 150	gca Ala	agc Ser	ggg Gly	gta Val	aca Thr	acc Thr 155	atg Met	att Ile	ggg Gly	ggc Gly 160	gga Gly	act Thr	ggg Gly	536
cct Pro	gct Ala	gat Asp 165	ggc Gly	act Thr	aat Asn	gcg Ala	act Thr 170	act Thr	atc Ile	act Thr	cca Pro	ggc Gly 175	aga Arg	aga Arg	aat Asn	584
tta Leu 180	aaa Lys	tgg Trp	atg Met	ctc Leu	aga Arg	gcg Ala 185	gct Ala	gaa Glu	gaa Glu	tat Tyr	tct Ser 190	atg Met	aac Asn	tta Leu	ggg Gly	632
ttc Phe 195	ttg Leu	gct Ala	aaa Lys	ggg Gly	aac Asn 200	gct Ala	tct Ser	aac Asn	gac Asp	gcg Ala 205	agc Ser	tta Leu	gcc Ala	gat Asp	caa Gln 210	680
att Ile	gaa Glu	gct Ala	ggg Gly	gcg Ala 215	att Ile	ggc Gly	ttt Phe	aaa Lys	atc Ile 220	cac His	gaa Glu	gac Asp	tgg Trp	ggc Gly 225	acc Thr	728
act Thr	cct Pro	tct Ser	gca Ala 230	atc Ile	aat Asn	cat His	gcg Ala	tta Leu 235	gat Asp	gtt Val	gca Ala	gac Asp	aaa Lys 240	tac Tyr	gat Asp	776
gtg Val	caa Gln 245	gtc Val	gct Ala	atc Ile	cac His	aca Thr	gac Asp 250	act Thr	ttg Leu	aat Asn	gaa Glu	gcc Ala 255	ggg Gly	tgc Cys	gtg Val	824
gaa Glu 260	gac Asp	act Thr	atg Met	gca Ala	gct Ala	att Ile 265	gcc Ala	gga Gly	cgc Arg	act Thr 270	atg Met	cac His	act Thr	ttc Phe	cac His	872

ccg gta aaa aat tgc aga aac atc act aaa aaa gac atg caa ttc aac 1640
 Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln Phe Asn
 515 520 525 530

gac act acc gct cac att gaa gtc aat cct gaa act tac cat gtg ttc 1688
 Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His Val Phe
 535 540 545

gtg gat ggc aaa gaa gta act tct aaa cca gcc aat aaa gtg agc ttg 1736
 Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val Ser Leu
 550 555 560

gcg caa ctc ttt agc att ttc taggattttt taggagcaac gctccttaaa 1787
 Ala Gln Leu Phe Ser Ile Phe
 565

tccttagttt ttagctctct gatttttt 1815

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 <212> PRT
 <213> Helicobacter pylori

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 Glu His Asp Tyr Thr Ile Tyr Gly Glu Glu Leu Lys Phe Gly Gly Gly
 35 40 45
 Lys Thr Leu Arg Glu Gly Met Ser Gln Ser Asn Asn Pro Ser Lys Glu
 50 55 60
 Glu Leu Asp Leu Ile Ile Thr Asn Ala Leu Ile Val Asp Tyr Thr Gly
 65 70 75 80
 Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile
 85 90 95
 Gly Lys Gly Gly Asn Lys Asp Met Gln Asp Gly Val Lys Asn Asn Leu
 100 105 110
 Ser Val Gly Gly Pro Ala Thr Glu Ala Leu Ala Gly Glu Gly Leu Ile Val
 115 120 125
 Thr Ala Gly Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln
 130 135 140
 Ile Pro Thr Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly
 145 150 155 160
 Thr Gly Pro Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg
 165 170 175
 Arg Asn Leu Lys Trp Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn
 180 185 190
 Leu Gly Phe Leu Ala Lys Gly Asn Ala Ser Asn Asp Ala Ser Leu Ala
 195 200 205
 Asp Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp
 210 215 220
 Gly Thr Thr Pro Ser Ala Ile Asn His Ala Leu Asp Val Ala Asp Lys
 225 230 235 240
 Tyr Asp Val Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly
 245 250 255
 Cys Val Glu Asp Thr Met Ala Ala Ile Ala Gly Arg Thr Met His Thr
 260 265 270

05895913-062901

Phe His Thr Glu Gly Ala Gly Gly Gly His Ala Pro Asp Ile Ile Lys
 275 280 285
 Val Ala Gly Glu His Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile
 290 295 300
 Pro Phe Thr Val Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val
 305 310 315 320
 Cys His His Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp
 325 330 335
 Ser Arg Ile Arg Pro Gln Thr Ile Ala Ala Glu Asp Thr Leu His Asp
 340 345 350
 Met Gly Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg
 355 360 365
 Val Gly Glu Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys
 370 375 380
 Lys Glu Phe Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe
 385 390 395 400
 Arg Ile Lys Arg Tyr Leu Ser Lys Tyr Thr Ile Asn Pro Ala Ile Ala
 405 410 415
 His Gly Ile Ser Glu Tyr Val Gly Ser Val Glu Val Gly Lys Val Ala
 420 425 430
 Asp Leu Val Leu Trp Ser Pro Ala Phe Phe Gly Val Lys Pro Asn Met
 435 440 445
 Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn
 450 455 460
 Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala
 465 470 475 480
 His His Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln
 485 490 495
 Ala Ala Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln
 500 505 510
 Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln
 515 520 525
 Phe Asn Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His
 530 535 540
 Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val
 545 550 555 560
 Ser Leu Ala Gln Leu Phe Ser Ile Phe
 565

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 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
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 atc gcg cat tct aat gaa atc gca cgc ccc att ttt aaa agc caa gac 104
 Ile Ala His Ser Asn Glu Ile Ala Arg Pro Ile Phe Lys Ser Gln Asp
 5 10 15
 cag ctt ttc act ctt tat caa ggg gat tgt aat gag gtt ttg ccc caa 152
 Gln Leu Phe Thr Leu Tyr Gln Gly Asp Cys Asn Glu Val Leu Pro Gln

20				25				30								
ttt	gaa	aac	cag	ttt	gat	ttg	att	ttt	gct	gat	ccg	cct	tat	ttc	ctc	200
Phe	Glu	Asn	Gln	Phe	Asp	Leu	Ile	Phe	Ala	Asp	Pro	Pro	Tyr	Phe	Leu	
35					40					45					50	
tct	aat	gac	ggc	tta	agc	ata	cag	agc	ggg	aaa	atc	gtg	agc	gtc	aat	248
Ser	Asn	Asp	Gly	Leu	Ser	Ile	Gln	Ser	Gly	Lys	Ile	Val	Ser	Val	Asn	
				55					60					65		
aaa	ggc	gat	tgg	gat	aaa	gaa	gat	ggg	att	aat	ggg	att	gat	gag	ttt	296
Lys	Gly	Asp	Trp	Asp	Lys	Glu	Asp	Gly	Ile	Asn	Gly	Ile	Asp	Glu	Phe	
			70					75					80			
aat	tac	cag	tgg	ata	aac	aac	gct	aaa	aag	gct	tta	aaa	gac	aca	gga	344
Asn	Tyr	Gln	Trp	Ile	Asn	Asn	Ala	Lys	Lys	Ala	Leu	Lys	Asp	Thr	Gly	
		85					90					95				
agc	ctt	tta	atc	agc	ggg	act	tac	cac	aac	atc	ttt	tct	ttg	ggg	tgt	392
Ser	Leu	Leu	Ile	Ser	Gly	Thr	Tyr	His	Asn	Ile	Phe	Ser	Leu	Gly	Cys	
	100					105					110					
gtt	tta	caa	aaa	ttg	gat	ttt	aag	att	tta	aac	ctc	atc	acc	tgg	caa	440
Val	Leu	Gln	Lys	Leu	Asp	Phe	Lys	Ile	Leu	Asn	Leu	Ile	Thr	Trp	Gln	
115					120					125					130	
aaa	acc	aac	cct	cct	ccc	aat	ttc	agc	tgc	cgt	tat	ttg	acg	cat	tca	488
Lys	Thr	Asn	Pro	Pro	Pro	Asn	Phe	Ser	Cys	Arg	Tyr	Leu	Thr	His	Ser	
				135					140					145		
gct	gag	caa	atc	att	tgg	gcg	aga	aaa	agc	cgc	aaa	cac	aag	cat	gtt	536
Ala	Glu	Gln	Ile	Ile	Trp	Ala	Arg	Lys	Ser	Arg	Lys	His	Lys	His	Val	
			150					155					160			
ttt	aac	tat	gag	gtt	tta	aaa	aag	atc	aat	aac	gac	aag	caa	atg	cgc	584
Phe	Asn	Tyr	Glu	Val	Leu	Lys	Lys	Ile	Asn	Asn	Asp	Lys	Gln	Met	Arg	
		165					170					175				
gat	gtg	tgg	agc	ttc	cca	gcg	atc	gct	cct	tgg	gaa	aaa	gtt	aat	ggc	632
Asp	Val	Trp	Ser	Phe	Pro	Ala	Ile	Ala	Pro	Trp	Glu	Lys	Val	Asn	Gly	
	180					185					190					
aag	cac	ccc	act	caa	aaa	ccc	ctc	gct	tta	tta	gtg	cgc	ttg	ctt	tta	680
Lys	His	Pro	Thr	Gln	Lys	Pro	Leu	Ala	Leu	Leu	Val	Arg	Leu	Leu	Leu	
195					200					205					210	
atg	gcg	agc	gat	gaa	aat	tct	ctc	att	ggc	gat	cct	ttt	agc	ggg	agc	728
Met	Ala	Ser	Asp	Glu	Asn	Ser	Leu	Ile	Gly	Asp	Pro	Phe	Ser	Gly	Ser	
				215					220					225		
tct	acc	aca	ggc	att	gcg	gct	aat	ctt	ttg	aag	agg	gaa	ttt	att	ggc	776
Ser	Thr	Thr	Gly	Ile	Ala	Ala	Asn	Leu	Leu	Lys	Arg	Glu	Phe	Ile	Gly	
			230					235					240			
ata	gaa	aaa	gaa	agc	gag											

Glu Leu Asp Ala Arg Tyr Lys Glu Ile Arg Ser Lys Ile Lys Asp Leu
 260 265 270

aac cac caa taaagccttt ttttaagcca cttaaagcgt tataacttttg
 Asn His Gln
 275

921

ggattttacc tca

934

<210> 254
 <211> 277
 <212> PRT
 <213> Helicobacter pylori

<400> 254
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 Pro Gln Phe Glu Asn Gln Phe Asp Leu Ile Phe Ala Asp Pro Pro Tyr
 35 40 45
 Phe Leu Ser Asn Asp Gly Leu Ser Ile Gln Ser Gly Lys Ile Val Ser
 50 55 60
 Val Asn Lys Gly Asp Trp Asp Lys Glu Asp Gly Ile Asn Gly Ile Asp
 65 70 75 80
 Glu Phe Asn Tyr Gln Trp Ile Asn Asn Ala Lys Lys Ala Leu Lys Asp
 85 90 95
 Thr Gly Ser Leu Leu Ile Ser Gly Thr Tyr His Asn Ile Phe Ser Leu
 100 105 110
 Gly Cys Val Leu Gln Lys Leu Asp Phe Lys Ile Leu Asn Leu Ile Thr
 115 120 125
 Trp Gln Lys Thr Asn Pro Pro Pro Asn Phe Ser Cys Arg Tyr Leu Thr
 130 135 140
 His Ser Ala Glu Gln Ile Ile Trp Ala Arg Lys Ser Arg Lys His Lys
 145 150 155 160
 His Val Phe Asn Tyr Glu Val Leu Lys Lys Ile Asn Asn Asp Lys Gln
 165 170 175
 Met Arg Asp Val Trp Ser Phe Pro Ala Ile Ala Pro Trp Glu Lys Val
 180 185 190
 Asn Gly Lys His Pro Thr Gln Lys Pro Leu Ala Leu Leu Val Arg Leu
 195 200 205
 Leu Leu Met Ala Ser Asp Glu Asn Ser Leu Ile Gly Asp Pro Phe Ser
 210 215 220
 Gly Ser Ser Thr Thr Gly Ile Ala Ala Asn Leu Leu Lys Arg Glu Phe
 225 230 235 240
 Ile Gly Ile Glu Lys Glu Ser Glu Phe Ile Lys Ile Ser Met Asp Arg
 245 250 255
 Lys Ile Glu Leu Asp Ala Arg Tyr Lys Glu Ile Arg Ser Lys Ile Lys
 260 265 270
 Asp Leu Asn His Gln
 275

<210> 255
 <211> 646
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS

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aatcaagcaa	accttcactc	tacccccccc	ccccccgaaa	ataataagaa	taataataaaa	120
aaagaggaag	aatatcagtg	caagctttct	ttgatttttag	ccgctaaaaa	cagcgtgttt	180
gtgcataataa	gaagagggga	ttatgtgggg	attggctgtc	agcttgggat	tgactatcaa	240
aaaaaggcgc	ttgagtat	atg gca aag	cgc gtg cca	aac atg gag	ctt ttt	291

gtg ttt tgc gaa gac tta gaa ttc acg caa aat ctt gat ctt ggc tac 339
Val Phe Cys Glu Asp Leu Glu Phe Thr Gln Asn Leu Asp Leu Gly Tyr
15 20 25

cct ttt atg gac atg acc act agg gat aaa gaa gaa gag gcg tat tgg 387
Pro Phe Met Asp Met Thr Thr Arg Asp Lys Glu Glu Glu Ala Tyr Trp
30 35 40

gac atg ctg ctc atg caa tct tgt cag cat ggc att atc gct aat agc 435
Asp Met Leu Leu Met Gln Ser Cys Gln His Gly Ile Ile Ala Asn Ser
45 50 55

act tat agc tgg tgg gcg gcc tat ttg ata gaa aat cca gaa aaa atc 483
Thr Tyr Ser Trp Trp Ala Ala Tyr Leu Ile Glu Asn Pro Glu Lys Ile
60 65 70 75

att att ggc ccc aaa cac tgg ctt ttt ggg cat gag aat atc ctt tgt 531
Ile Ile Gly Pro Lys His Trp Leu Phe Gly His Glu Asn Ile Leu Cys
80 85 90

aag gag tgg gtg aaa ata gaa tcc cat ttt gag gta aaa tcc caa aag 579
Lys Glu Trp Val Lys Ile Glu Ser His Phe Glu Val Lys Ser Gln Lys
95 100 105

tat aac gct taaagtggct taaaaaagg ctttattggt ggtttaaadc 628
Tyr Asn Ala
110

tttgatttta gatcggat 646

$\langle 211 \rangle$ 110

<213> Helicobacter pylori

Met	Ala	Lys	Arg	Val	Pro	Asn	Met	Glu	Leu	Phe	Val	Phe	Cys	Glu	Asp
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Leu	Glu	Phe	Thr	Gln	Asn	Leu	Asp	Leu	Gly	Tyr	Pro	Phe	Met	Asp	Met
			20					25					30		
Thr	Thr	Arg	Asp	Lys	Glu	Glu	Glu	Ala	Tyr	Trp	Asp	Met	Leu	Leu	Met
			35				40					45			
Gln	Ser	Cys	Gln	His	Gly	Ile	Ile	Ala	Asn	Ser	Thr	Tyr	Ser	Trp	Trp
	50					55					60				
Ala	Ala	Tyr	Leu	Ile	Glu	Asn	Pro	Glu	Lys	Ile	Ile	Ile	Gly	Pro	Lys
65					70					75				80	
His	Trp	Leu	Phe	Gly	His	Glu	Asn	Ile	Leu	Cys	Lys	Glu	Trp	Val	Lys
				85					90					95	

Ile Glu Ser His Phe Glu Val Lys Ser Gln Lys Tyr Asn Ala
 100 105 110

<210> 257
 <211> 1027
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(974)

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 aaa gaa aat ccg cct atc gtt ttt ggg cct gtt tta tcc agg cgt ttt 104
 Lys Glu Asn Pro Pro Ile Val Phe Gly Pro Val Leu Ser Arg Arg Phe
 5 10 15
 ggg aag tct ttg ggc gtg gat cta tcg ccc tct aaa aaa caa tgc aat 152
 Gly Lys Ser Leu Gly Val Asp Leu Ser Pro Ser Lys Lys Gln Cys Asn
 20 25 30
 tac aat tgc att tat tgc gag ttg ggt aaa gcc aag ccc att gaa cgc 200
 Tyr Asn Cys Ile Tyr Cys Glu Leu Gly Lys Ala Lys Pro Ile Glu Arg
 35 40 45 50
 atg gaa gaa gtg atc aaa gtg gaa acc ttg att aac gcc att caa aac 248
 Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile Gln Asn
 55 60 65
 gcc cta aac aac ctc acc acc ccc att gat gtt tta acc att acc gct 296
 Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile Thr Ala
 70 75 80
 aat ggc gaa ccc acg cta tac cct cat tta tta gag ctt atc caa agc 344
 Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile Gln Ser
 85 90 95
 atc aag cct ttt tta aag ggc gtt aaa act ttg att tta agc aat ggc 392
 Ile Lys Pro Phe Leu Lys Gly Val Lys Thr Leu Ile Leu Ser Asn Gly
 100 105 110
 tcg ctc ttt tat gag cca aaa gtc cag caa gcc tta aag gaa ttt gac 440
 Ser Leu Phe Tyr Glu Pro Lys Val Gln Gln Ala Leu Lys Glu Phe Asp
 115 120 125 130
 atc gtt aaa ttt tct tta gac gct att gat ttg aaa gcc ttt gaa aga 488
 Ile Val Lys Phe Ser Leu Asp Ala Ile Asp Leu Lys Ala Phe Glu Arg
 135 140 145
 gtg gat aaa ccc tat tct aaa gac att aat aag att tta gag ggg att 536
 Val Asp Lys Pro Tyr Ser Lys Asp Ile Asn Lys Ile Leu Glu Gly Ile
 150 155 160
 ttg cgc ttt tct caa att tat caa ggg caa ttg gtg gct gaa gtg ttg 584
 Leu Arg Phe Ser Gln Ile Tyr Gln Gly Gln Leu Val Ala Glu Val Leu

165	170	175	
tta att aag ggc gtg aat gat agc gcg aac aac tta aaa ctc atc gct Leu Ile Lys Gly Val Asn Asp Ser Ala Asn Asn Leu Lys Leu Ile Ala 180 185 190			632
gcc ttt tta aaa caa atc aat ata gcc aga gtg gat tta agc acc ata Ala Phe Leu Lys Gln Ile Asn Ile Ala Arg Val Asp Leu Ser Thr Ile 195 200 205 210			680
gac aga ccc tca agc ttt aaa gcc cct aaa tta agc gaa gat gaa ttg Asp Arg Pro Ser Ser Phe Lys Ala Pro Lys Leu Ser Glu Asp Glu Leu 215 220 225			728
tta aaa tgc tct tta ttt ttt gaa ggg ctt tgc gtg agt ttg cct aaa Leu Lys Cys Ser Leu Phe Phe Glu Gly Leu Cys Val Ser Leu Pro Lys 230 235 240			776
cga tcc att act caa gct aaa aaa ttg att tct tgc ggt ata gac gaa Arg Ser Ile Thr Gln Ala Lys Lys Leu Ile Ser Cys Gly Ile Asp Glu 245 250 255			824
ttg ctc gct tta att tcc agg cgc cct tta agc gca gaa gaa gcc ccc Leu Leu Ala Leu Ile Ser Arg Arg Pro Leu Ser Ala Glu Glu Ala Pro 260 265 270			872
cta att cta gat tct aac gct ttt aag cat tta gaa act ttg tta aac Leu Ile Leu Asp Ser Asn Ala Phe Lys His Leu Glu Thr Leu Leu Asn 275 280 285 290			920
cat aag caa att acg att aaa aaa gtc ggc tct ttg gag ttt tat tgc His Lys Gln Ile Thr Ile Lys Lys Val Gly Ser Leu Glu Phe Tyr Cys 295 300 305			968
gcg ttt taacctccat ttgtaagttt taccttactt tagggatagc ttaagctttt Ala Phe			1024
aaa			1027
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<211> 308			
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Arg Phe Gly Lys Ser Leu Gly Val Asp Leu Ser Pro Ser Lys Lys Gln 20 25 30			
Cys Asn Tyr Asn Cys Ile Tyr Cys Glu Leu Gly Lys Ala Lys Pro Ile 35 40 45			
Glu Arg Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile 50 55 60			
Gln Asn Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile 65 70 75 80			
Thr Ala Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile 85 90 95			
Gln Ser Ile Lys Pro Phe Leu Lys Gly Val Lys Thr Leu Ile Leu Ser			

Asn Gly Ser	100	Pro Lys Val	105	Gln Gln Ala	110	Leu Lys Glu
Phe Asp Ile	115	Leu Asp Ala	120	Ile Asp Leu	125	Lys Ala Phe
Glu Arg Val	130	Ser Lys Asp	135	Ile Asn Lys	140	Ile Leu Glu
Gly Ile Leu	145	Arg Phe Ser	150	Gln Gly Gln	155	Leu Val Ala
Val Leu Leu	165	Ile Lys Gly	170	Val Asn Asp	175	Leu Lys Leu
Ile Ala Ala	180	Phe Leu Lys	185	Gln Ile Asn	190	Ile Ala Arg
Thr Ile Asp	195	Arg Pro Ser	200	Val Asn Ile	205	Val Asp Leu
Glu Leu Leu	210	Lys Cys Ser	215	Leu Phe Phe	220	Lys Leu Ser
Pro Lys Arg	225	Ser Ile Thr	230	Glu Gly Leu	235	Cys Val Ser
Asp Glu Leu	245	Leu Ala Leu	250	Ile Ser Cys	255	Gly Ile Glu
Ala Pro Leu	260	Ile Leu Asp	265	Arg Arg Pro	270	Leu Ser Ala
Leu Asn His	275	Lys Gln Ile	280	Thr Asn Ala	285	Phe Lys His
Tyr Cys Ala	290	Phe Tyr Ser	295	Gly Val Gly	300	Ser Leu Glu
	305					

<210> 259
 <211> 1350
 <212> DNA
 <213> Helicobacter pylori
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 <222> (87)...(1280)

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Met Glu Ser Val Lys Thr Gly Lys Thr	
1 5	
aat aag gtt ggc aag aat aca gag atg gct aat aca aag gca aat aaa	161
Asn Lys Val Gly Lys Asn Thr Glu Met Ala Asn Thr Lys Ala Asn Lys	
10 15 20 25	
gag act cat ttt aaa caa gtg agc gcc att aca aat ata atc aga tca	209
Glu Thr His Phe Lys Gln Val Ser Ala Ile Thr Asn Ile Ile Arg Ser	
30 35 40	
gtt ggt ggg ttt ttt aca aaa att gca aag aga gtt aga gga ctt gta	257
Val Gly Gly Phe Phe Thr Lys Ile Ala Lys Arg Val Arg Gly Leu Val	
45 50 55	
aaa aaa cac ccc aag aaa agc agt gcg gca tta gta gta ttg acc cat	305
Lys Lys His Pro Lys Lys Ser Ser Ala Ala Leu Val Val Leu Thr His	
60 65 70	

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att gcg tgc aag aaa gcg aaa gaa tta gac gat aaa gtc caa gat aaa Ile Ala Cys Lys Lys Ala Lys Glu Leu Asp Asp Lys Val Gln Asp Lys 75 80 85	353
tcc aaa caa gct gaa aaa gaa aat caa atc aat tgg tgg aaa tat tca Ser Lys Gln Ala Glu Lys Glu Asn Gln Ile Asn Trp Trp Lys Tyr Ser 90 95 100 105	401
gga tta aca ata gcg gca agt tta tta tta gcc gct tgt agc gct ggt Gly Leu Thr Ile Ala Ala Ser Leu Leu Leu Ala Ala Cys Ser Ala Gly 110 115 120	449
gat act gat aaa cag ata gaa cta gaa caa gaa aaa aag gaa gct gaa Asp Thr Asp Lys Gln Ile Glu Leu Glu Gln Glu Lys Lys Glu Ala Glu 125 130 135	497
aac gct agg gat aga gcg aac aag agt ggg ata gaa cta gaa caa gaa Asn Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu 140 145 150	545
aga cag aaa aca aac aag agt ggg ata gaa ctc gct aat agt caa ata Arg Gln Lys Thr Asn Lys Ser Gly Ile Glu Leu Ala Asn Ser Gln Ile 155 160 165	593
aaa gca gaa caa gaa aga caa aag aca gaa caa gaa aaa caa aaa gca Lys Ala Glu Gln Glu Arg Gln Lys Thr Glu Gln Glu Lys Gln Lys Ala 170 175 180 185	641
aat aag agt gcg ata gag tta gaa cag caa aaa caa aag acc att aat Asn Lys Ser Ala Ile Glu Leu Glu Gln Gln Lys Gln Lys Thr Ile Asn 190 195 200	689
aca caa aga gat ttg att aaa gaa cag aaa gat ttc att aaa gaa aca Thr Gln Arg Asp Leu Ile Lys Glu Gln Lys Asp Phe Ile Lys Glu Thr 205 210 215	737
gaa caa aat tgc caa gaa aat cat aat caa ttc ttt att aaa aaa tta Glu Gln Asn Cys Gln Glu Asn His Asn Gln Phe Phe Ile Lys Lys Leu 220 225 230	785
gga att aag ggt ggc att gct ata gaa gta gaa gct gaa tgc aaa acc Gly Ile Lys Gly Gly Ile Ala Ile Glu Val Glu Ala Glu Cys Lys Thr 235 240 245	833
cct aaa cct gca aaa acc aat caa acc cct atc cag cca aaa cac ctc Pro Lys Pro Ala Lys Thr Asn Gln Thr Pro Ile Gln Pro Lys His Leu 250 255 260 265	881
cca aac tct aaa caa cct cat tct caa aga gga tca aaa gcg caa gag Pro Asn Ser Lys Gln Pro His Ser Gln Arg Gly Ser Lys Ala Gln Glu 270 275 280	929
ttt atc gct tat ttg caa aaa gag cta gaa ttt ctg ccc tat tcg caa Phe Ile Ala Tyr Leu Gln Lys Glu Leu Glu Phe Leu Pro Tyr Ser Gln 285 290 295	977
aaa gct atc gct aaa caa gtg aat ttc tat aaa cca agt tct atc gct Lys Ala Ile Ala Lys Gln Val Asn Phe Tyr Lys Pro Ser Ser Ile Ala 300 305 310	1025

Glu Gln Lys Asp Phe Ile Lys Glu Thr Glu Gln Asn Cys Gln Glu Asn
 210 215 220
 His Asn Gln Phe Phe Ile Lys Lys Leu Gly Ile Lys Gly Gly Ile Ala
 225 230 235 240
 Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn
 245 250 255
 Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro His
 260 265 270
 Ser Gln Arg Gly Ser Lys Ala Gln Glu Phe Ile Ala Tyr Leu Gln Lys
 275 280 285
 Glu Leu Glu Phe Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val
 290 295 300
 Asn Phe Tyr Lys Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro Arg
 305 310 315 320
 Asp Phe Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg
 325 330 335
 Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Asp Leu Lys Pro Asp
 340 345 350
 Pro Gln Ala His Leu Pro Thr Ser Gln Ser Leu Leu Phe Val Gln Lys
 355 360 365
 Ile Phe Ala Asp Val Asn Lys Glu Ile Glu Ala Val Ala Asn Thr Glu
 370 375 380
 Lys Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met
 385 390 395

<210> 261
 <211> 1939
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1886)

<400> 261
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 Met Ser
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 gcg gaa ctg att gct gtt tat aaa gac gag caa ata ata gat tta gag 104
 Ala Glu Leu Ile Ala Val Tyr Lys Asp Glu Gln Ile Ile Asp Leu Glu
 5 10 15
 agc gcg aaa gtc tta ggg ctg agc gat ggg att aaa gcg tta aac ggg 152
 Ser Ala Lys Val Leu Gly Leu Ser Asp Gly Ile Lys Ala Leu Asn Gly
 20 25 30
 aca gag ccg ata tat ttt gat gat tcg cct ttg gct tta gag gtg att 200
 Thr Glu Pro Ile Tyr Phe Asp Asp Ser Pro Leu Ala Leu Glu Val Ile
 35 40 45 50
 agg cat tca tgc gcg cat ttg ctt gcg caa agc ttg aaa gcc ctt tat 248
 Arg His Ser Cys Ala His Leu Leu Ala Gln Ser Leu Lys Ala Leu Tyr
 55 60 65
 ccg gac gcg aaa ttt ttt gta ggc cct gtg gta gaa gag ggg ttt tat 296
 Pro Asp Ala Lys Phe Phe Val Gly Pro Val Val Glu Glu Gly Phe Tyr
 70 75 80

tac gat ttc aag act tct tca aaa atc agc gaa gag gat ttg cct aaa	344
Tyr Asp Phe Lys Thr Ser Ser Lys Ile Ser Glu Glu Asp Leu Pro Lys	
85 90 95	
att gaa gcg aaa atg aaa gag ttt gcg aag ttg aaa ctc gct atc act	392
Ile Glu Ala Lys Met Lys Glu Phe Ala Lys Leu Lys Leu Ala Ile Thr	
100 105 110	
aaa gag act tta acc aga gag caa gct ttg gag cgt ttt aag ggc gat	440
Lys Glu Thr Leu Thr Arg Glu Gln Ala Leu Glu Arg Phe Lys Gly Asp	
115 120 125 130	
gaa tta aag cat gcg gtg atg agt aaa atc ggt ggc gat gcc ttt ggc	488
Glu Leu Lys His Ala Val Met Ser Lys Ile Gly Gly Asp Ala Phe Gly	
135 140 145	
gtg tat caa caa ggc gag ttt gaa gat ttg tgt aag ggg ccg cat ctc	536
Val Tyr Gln Gln Gly Glu Phe Glu Asp Leu Cys Lys Gly Pro His Leu	
150 155 160	
cca aac acc cgt ttt tta aac cat ttt aag ctc act aaa ctg gct ggg	584
Pro Asn Thr Arg Phe Leu Asn His Phe Lys Leu Thr Lys Leu Ala Gly	
165 170 175	
gct tat ttg ggc ggc gat gaa aac aat gaa atg ctc att aga atc tat	632
Ala Tyr Leu Gly Gly Asp Glu Asn Asn Glu Met Leu Ile Arg Ile Tyr	
180 185 190	
gga atc gct ttt gcc acc aaa gag ggt tta aaa gac tat ctt ttc caa	680
Gly Ile Ala Phe Ala Thr Lys Glu Gly Leu Lys Asp Tyr Leu Phe Gln	
195 200 205 210	
ata gaa gaa gcg aaa aaa cga gat cac aga aag cta ggc gtg gag cta	728
Ile Glu Glu Ala Lys Lys Arg Asp His Arg Lys Leu Gly Val Glu Leu	
215 220 225	
ggg ctt ttt agc ttt gat gat gag ata ggg gcg ggc tta cct tta tgg	776
Gly Leu Phe Ser Phe Asp Asp Glu Ile Gly Ala Gly Leu Pro Leu Trp	
230 235 240	
ctg cct aaa ggg gca agg ctt agg aag cgc att gaa gat tta ttg agt	824
Leu Pro Lys Gly Ala Arg Leu Arg Lys Arg Ile Glu Asp Leu Leu Ser	
245 250 255	
caa gcg tta ctt tta aga ggc tat gag ccg gtt aaa ggt cct gag att	872
Gln Ala Leu Leu Leu Arg Gly Tyr Glu Pro Val Lys Gly Pro Glu Ile	
260 265 270	
tta aag agc gat gtg tgg aaa atc agc ggg cat tat gac aac tat aaa	920
Leu Lys Ser Asp Val Trp Lys Ile Ser Gly His Tyr Asp Asn Tyr Lys	
275 280 285 290	
gaa aac atg tat ttc acc acg att gat gag caa gaa tat ggc ata aag	968
Glu Asn Met Tyr Phe Thr Thr Ile Asp Glu Gln Glu Tyr Gly Ile Lys	
295 300 305	
cct atg aac tgc gtg ggg cat att aaa gtc tat caa agc gct ttg cac	1016
Pro Met Asn Cys Val Gly His Ile Lys Val Tyr Gln Ser Ala Leu His	
310 315 320	

agc tac aga gat ttg ccc tta agg ttt tat gaa tac ggc gtg gtg cat	1064
Ser Tyr Arg Asp Leu Pro Leu Arg Phe Tyr Glu Tyr Gly Val Val His	
325 330 335	
cgg cat gaa aaa agc ggc gtg ttg cat ggg ctt tta agg gtt agg gaa	1112
Arg His Glu Lys Ser Gly Val Leu His Gly Leu Leu Arg Val Arg Glu	
340 345 350	
ttt acc caa gat gat gca cat att ttt tgc tct ttt gaa cag atc caa	1160
Phe Thr Gln Asp Asp Ala His Ile Phe Cys Ser Phe Glu Gln Ile Gln	
355 360 365 370	
agc gaa gtg agc gcg att tta gat ttt acg cac aaa atc atg caa gcg	1208
Ser Glu Val Ser Ala Ile Leu Asp Phe Thr His Lys Ile Met Gln Ala	
375 380 385	
ttt gat ttt agc tat gaa atg gaa tta tcc aca agg ccg gct aaa tcc	1256
Phe Asp Phe Ser Tyr Glu Met Glu Leu Ser Thr Arg Pro Ala Lys Ser	
390 395 400	
ata ggc gat gat aaa gtt tgg gaa aag gcc act aac gct tta aaa gaa	1304
Ile Gly Asp Asp Lys Val Trp Glu Lys Ala Thr Asn Ala Leu Lys Glu	
405 410 415	
gcc tta aaa gaa cac cgc att gat tac aag att gat gaa ggg gga ggg	1352
Ala Leu Lys Glu His Arg Ile Asp Tyr Lys Ile Asp Glu Gly Gly Gly	
420 425 430	
gct ttc tat ggg cct aag att gac att aaa atc act gac gct tta aag	1400
Ala Phe Tyr Gly Pro Lys Ile Asp Ile Lys Ile Thr Asp Ala Leu Lys	
435 440 445 450	
cgt aaa tgg cag tgt ggc acg att caa gtg gat atg aat ttg cct gaa	1448
Arg Lys Trp Gln Cys Gly Thr Ile Gln Val Asp Met Asn Leu Pro Glu	
455 460 465	
cgc ttc aag ctc gct ttc act aat gag tat aat cac gct gag cag ccg	1496
Arg Phe Lys Leu Ala Phe Thr Asn Glu Tyr Asn His Ala Glu Gln Pro	
470 475 480	
gtg atg atc cac aga gcg att tta ggc tcg ttt gaa agg ttt att gcg	1544
Val Met Ile His Arg Ala Ile Leu Gly Ser Phe Glu Arg Phe Ile Ala	
485 490 495	
att ttg agc gaa cat ttt ggg ggg aat ttc cct ttc ttt gtc gcg ccc	1592
Ile Leu Ser Glu His Phe Gly Gly Asn Phe Pro Phe Phe Val Ala Pro	
500 505 510	
act caa atc gct ctc atc cct att aat gaa gag cat cat gtt ttt gct	1640
Thr Gln Ile Ala Leu Ile Pro Ile Asn Glu Glu His His Val Phe Ala	
515 520 525 530	
ttg aaa tta aaa gag gcg cta aaa aag cgc gat att ttt gta gaa gtg	1688
Leu Lys Leu Lys Glu Ala Leu Lys Lys Arg Asp Ile Phe Val Glu Val	
535 540 545	
tta gat aaa aac gac agc ttg aat aaa aag gtg cga tta gcc gaa aag	1736
Leu Asp Lys Asn Asp Ser Leu Asn Lys Lys Val Arg Leu Ala Glu Lys	

	260		265		270
Glu Ile Leu Lys Ser Asp Val Trp Lys Ile Ser Gly His Tyr Asp Asn					
	275		280		285
Tyr Lys Glu Asn Met Tyr Phe Thr Thr Ile Asp Glu Gln Glu Tyr Gly					
	290		295		300
Ile Lys Pro Met Asn Cys Val Gly His Ile Lys Val Tyr Gln Ser Ala					
305		310		315	320
Leu His Ser Tyr Arg Asp Leu Pro Leu Arg Phe Tyr Glu Tyr Gly Val					
	325		330		335
Val His Arg His Glu Lys Ser Gly Val Leu His Gly Leu Leu Arg Val					
	340		345		350
Arg Glu Phe Thr Gln Asp Asp Ala His Ile Phe Cys Ser Phe Glu Gln					
	355		360		365
Ile Gln Ser Glu Val Ser Ala Ile Leu Asp Phe Thr His Lys Ile Met					
	370		375		380
Gln Ala Phe Asp Phe Ser Tyr Glu Met Glu Leu Ser Thr Arg Pro Ala					
385		390		395	400
Lys Ser Ile Gly Asp Asp Lys Val Trp Glu Lys Ala Thr Asn Ala Leu					
	405		410		415
Lys Glu Ala Leu Lys Glu His Arg Ile Asp Tyr Lys Ile Asp Glu Gly					
	420		425		430
Gly Gly Ala Phe Tyr Gly Pro Lys Ile Asp Ile Lys Ile Thr Asp Ala					
	435		440		445
Leu Lys Arg Lys Trp Gln Cys Gly Thr Ile Gln Val Asp Met Asn Leu					
	450		455		460
Pro Glu Arg Phe Lys Leu Ala Phe Thr Asn Glu Tyr Asn His Ala Glu					
465		470		475	480
Gln Pro Val Met Ile His Arg Ala Ile Leu Gly Ser Phe Glu Arg Phe					
	485		490		495
Ile Ala Ile Leu Ser Glu His Phe Gly Asn Phe Pro Phe Phe Val					
	500		505		510
Ala Pro Thr Gln Ile Ala Leu Ile Pro Ile Asn Glu Glu His His Val					
	515		520		525
Phe Ala Leu Lys Leu Lys Glu Ala Leu Lys Lys Arg Asp Ile Phe Val					
	530		535		540
Glu Val Leu Asp Lys Asn Asp Ser Leu Asn Lys Lys Val Arg Leu Ala					
545		550		555	560
Glu Lys Gln Lys Ile Pro Met Ile Leu Val Leu Gly Asn Glu Glu Val					
	565		570		575
Glu Thr Glu Ile Leu Ser Ile Arg Asp Arg Glu Lys Gln Asp Gln Tyr					
	580		585		590
Lys Met Pro Leu Lys Glu Phe Leu Asn Met Val Glu Ser Lys Met Gln					
	595		600		605
Glu Val Ser Phe					
610					

<210> 263
 <211> 1198
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1145)

<400> 263
 gcgattgtgc ggagtcgttt tctcaattta gcgccaatcg gattagagac atg ttt
 Met Phe
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aaa gta atg atg caa atg gcg atc gtt ctc act ttt gct ggc tct ata	104
Lys Val Met Met Gln Met Ala Ile Val Leu Thr Phe Ala Gly Ser Ile	
5 10 15	
ccg atc gtg aaa gtg ggg cgc att gcc ggg caa ttt gcc aag cct cgc	152
Pro Ile Val Lys Val Gly Arg Ile Ala Gly Gln Phe Ala Lys Pro Arg	
20 25 30	
tcc aat gcg act gaa atg ctg gat aat gaa gaa gtg ttg agt tac aga	200
Ser Asn Ala Thr Glu Met Leu Asp Asn Glu Glu Val Leu Ser Tyr Arg	
35 40 45 50	
ggg gat att atc aat ggg att tcc aaa aaa gaa aga gag cca aat cct	248
Gly Asp Ile Ile Asn Gly Ile Ser Lys Lys Glu Arg Glu Pro Asn Pro	
55 60 65	
gaa aga atg ctt aag gcc tac cat caa agc gta gcg act tta aac ctt	296
Glu Arg Met Leu Lys Ala Tyr His Gln Ser Val Ala Thr Leu Asn Leu	
70 75 80	
atc aga gcc ttt gct caa ggc ggg tta gcg gat ttg gag caa gtg cat	344
Ile Arg Ala Phe Ala Gln Gly Leu Ala Asp Leu Glu Gln Val His	
85 90 95	
cgt ttc aat ttg gat ttt gtc aaa aac aac gac ttt ggg caa aaa tac	392
Arg Phe Asn Leu Asp Phe Val Lys Asn Asn Asp Phe Gly Gln Lys Tyr	
100 105 110	
cag caa atc gct gac cgg atc acg caa gct tta ggg ttt atg cga gca	440
Gln Gln Ile Ala Asp Arg Ile Thr Gln Ala Leu Gly Phe Met Arg Ala	
115 120 125 130	
tgc ggg gtg gag ata gag cga acg cct att ctt agg gaa gtg gaa ttt	488
Cys Gly Val Glu Ile Glu Arg Thr Pro Ile Leu Arg Glu Val Glu Phe	
135 140 145	
tac acc agc cac gaa gcg tta ctg ctc cat tat gaa gag ccg ttg gtg	536
Tyr Thr Ser His Glu Ala Leu Leu His Tyr Glu Glu Pro Leu Val	
150 155 160	
cgt aag gat agt ctg act aac cag ttt tat gat tgc tcc gcg cac atg	584
Arg Lys Asp Ser Leu Thr Asn Gln Phe Tyr Asp Cys Ser Ala His Met	
165 170 175	
cta tgg att ggc gaa agg aca aga gac cct aag ggt gcg cat gtg gag	632
Leu Trp Ile Gly Glu Arg Thr Arg Asp Pro Lys Gly Ala His Val Glu	
180 185 190	
ttt tta agg ggg gtt tgt aac cct att ggc gtg aaa atc ggg cct aat	680
Phe Leu Arg Gly Val Cys Asn Pro Ile Gly Val Lys Ile Gly Pro Asn	
195 200 205 210	
gcg agc gtg agc gaa gtg tta gaa ttg tgc gat gtt tta aac ccg cgc	728
Ala Ser Val Ser Glu Val Leu Glu Leu Cys Asp Val Leu Asn Pro Arg	
215 220 225	
aac att aag ggg cgt ttg aat ttg atc gtg cgc atg ggt tct aag atg	776
Asn Ile Lys Gly Arg Leu Asn Leu Ile Val Arg Met Gly Ser Lys Met	

[illegible]

<400> 264															
Met 1	Phe	Lys	Val	Met 5	Met	Gln	Met	Ala	Ile 10	Val	Leu	Thr	Phe	Ala 15	Gly
Ser	Ile	Pro	Ile 20	Val	Lys	Val	Gly	Arg 25	Ile	Ala	Gly	Gln	Phe 30	Ala	Lys
Pro	Arg	Ser 35	Asn	Ala	Thr	Glu	Met 40	Leu	Asp	Asn	Glu	Glu 45	Val	Leu	Ser
Tyr 50	Arg	Gly	Asp	Ile	Ile 55	Asn	Gly	Ile	Ser	Lys	Lys 60	Glu	Arg	Glu	Pro
Asn 65	Pro	Glu	Arg	Met 70	Leu	Lys	Ala	Tyr	His 75	Gln	Ser	Val	Ala	Thr 80	Leu
Asn	Leu	Ile	Arg 85	Ala	Phe	Ala	Gln	Gly	Gly 90	Leu	Ala	Asp	Leu 95	Glu	Gln
Val	His	Arg	Phe 100	Asn	Leu	Asp	Phe 105	Val	Lys	Asn	Asn	Asp	Phe 110	Gly	Gln
Lys	Tyr	Gln 115	Gln	Ile	Ala	Asp	Arg 120	Ile	Thr	Gln	Ala	Leu 125	Gly	Phe	Met
Arg	Ala	Cys	Gly	Val	Glu	Ile	Glu	Arg	Thr	Pro	Ile	Leu	Arg	Glu	Val

130	135	140
Glu Phe Tyr Thr Ser His	Glu Ala Leu Leu Leu	His Tyr Glu Glu Pro
145	150	155
Leu Val Arg Lys Asp Ser	Leu Thr Asn Gln Phe	Tyr Asp Cys Ser Ala
165	170	175
His Met Leu Trp Ile Gly	Glu Arg Thr Arg Asp	Pro Lys Gly Ala His
180	185	190
Val Glu Phe Leu Arg Gly	Val Cys Asn Pro Ile	Gly Val Lys Ile Gly
195	200	205
Pro Asn Ala Ser Val Ser	Glu Val Leu Glu Leu	Cys Asp Val Leu Asn
210	215	220
Pro Arg Asn Ile Lys Gly	Arg Leu Asn Leu Ile	Val Arg Met Gly Ser
225	230	235
Lys Met Ile Lys Glu Arg	Leu Pro Lys Leu Leu	Gln Gly Val Leu Glu
245	250	255
Glu Lys Arg His Ile Leu	Trp Ser Ile Asp Pro	Met His Gly Asn Thr
260	265	270
Val Lys Thr Ser Leu Gly	Val Lys Thr Arg Ala	Phe Asp Ser Val Leu
275	280	285
Asp Glu Val Lys Ser Phe	Phe Glu Ile His Arg	Ala Glu Gly Ser Leu
290	295	300
Ala Ser Gly Val His Leu	Glu Met Thr Gly Glu	Asn Val Thr Glu Cys
305	310	315
Ile Gly Gly Ser Gln Ala	Ile Thr Glu Glu Gly	Leu Ser Cys His Tyr
325	330	335
Tyr Thr Gln Cys Asp Pro	Arg Leu Asn Ala Thr	Gln Ala Leu Glu Leu
340	345	350
Ala Phe Leu Ile Ala Asp	Met Leu Lys Lys Gln	His Ala
355	360	365

<210> 265
 <211> 388
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(335)

<400> 265	
tgatagcgac tttttgaggc ccatgcaccc caaaaacggt ttttaattca atg tca	56
Met Ser	
1	
gct gtc cgg cta ggc ccg cca ata agg agc atg ttt gtg ggt aat gca	104
Ala Val Arg Leu Gly Pro Pro Ile Arg Ser Met Phe Val Gly Asn Ala	
5 10 15	
ccg ttt tgg ctt tgg ttt ttt aaa gct tgc atg cct tca ctc aaa ttg	152
Pro Phe Trp Leu Trp Phe Phe Lys Ala Cys Met Pro Ser Leu Lys Leu	
20 25 30	
cgc aca atg gat tct ttt ttc aat aag atg atg caa tta agg gtg atg	200
Arg Thr Met Asp Ser Phe Phe Asn Lys Met Met Gln Leu Arg Val Met	
35 40 45 50	
agc gaa agc aat cgc ggg ctt gca tgc gaa gag acc gcc cca atc atg	248
Ser Glu Ser Asn Arg Gly Leu Ala Cys Glu Glu Thr Ala Pro Ile Met	
55 60 65	

106290-ET56860

ccc aag ctt gaa atc cca caa acc cca tgc aat aaa gcc gta tca atc 296
Pro Lys Leu Glu Ile Pro Gln Thr Pro Cys Asn Lys Ala Val Ser Ile
70 75 80

tca aac aac tct tca cgc atc gct tca att tct tta tca taaggctgta 345
Ser Asn Asn Ser Ser Arg Ile Ala Ser Ile Ser Leu Ser
85 90 95

aagtaaaatc cttaaagcgt tcaaaattca aattcaaadc tgt 388

<210> 266

<211> 95

<212> PRT

<213> Helicobacter pylori

<400> 266

Met Ser Ala Val Arg Leu Gly Pro Pro Ile Arg Ser Met Phe Val Gly
1 5 10 15
Asn Ala Pro Phe Trp Leu Trp Phe Phe Lys Ala Cys Met Pro Ser Leu
20 25 30
Lys Leu Arg Thr Met Asp Ser Phe Asn Lys Met Met Gln Leu Arg
35 40 45
Val Met Ser Glu Ser Asn Arg Gly Leu Ala Cys Glu Glu Thr Ala Pro
50 55 60
Ile Met Pro Lys Leu Glu Ile Pro Gln Thr Pro Cys Asn Lys Ala Val
65 70 75 80
Ser Ile Ser Asn Asn Ser Ser Arg Ile Ala Ser Ile Ser Leu Ser
85 90 95

<210> 267

<211> 1756

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1703)

<400> 267

ttttaagag aactagcact aagagaatat ttttaaaaag ggatttttta gtg cta 56
Val Leu
1

gaa ttt cat caa att tat gat cct ttg ggt aat att tgg ctg agc gct 104
Glu Phe His Gln Ile Tyr Asp Pro Leu Gly Asn Ile Trp Leu Ser Ala
5 10 15

ctt gtg gcc tta ttg ccg att tta ttg ttt ttc tta tct tta atg gtt 152
Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu Met Val
20 25 30

ttt aaa ctc aaa ggt tat aca gcg gcc ttt ttg agc gtg gcc tta tca 200
Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala Leu Ser
35 40 45 50

gcc gtt att gcg gtt tta gtg tat aaa atg cct gtt agc atg gtg ggt 248
Ala Val Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met Val Gly
55 60 65

	295	300	305	
gtg att gtg cta tgg ata cag cct ttt ttt aaa gcc ttg ttt gaa aaa	1016			
Val Ile Val Leu Trp Ile Gln Pro Phe Phe Lys Ala Leu Phe Glu Lys	310	315	320	
gac ggc ttg tta gct ttt tct aat ttt tat ttt gaa ttc aat aac atc	1064			
Asp Gly Leu Leu Ala Phe Ser Asn Phe Tyr Phe Glu Phe Asn Asn Ile	325	330	335	
agt aac cac atc ttt aaa agc ccg cct ttt gta gaa gcc aat caa agc	1112			
Ser Asn His Ile Phe Lys Ser Pro Pro Phe Val Glu Ala Asn Gln Ser	340	345	350	
gtg agt ttt ccg gtg gtg ttt aaa ttt ctc tta atc aac acg gtt ggc	1160			
Val Ser Phe Pro Val Val Phe Lys Phe Leu Leu Ile Asn Thr Val Gly	355	360	365	370
act tcc att ttt tta gcc gct ctt gtt agc atg ctc gtt tta agg gtg	1208			
Thr Ser Ile Phe Leu Ala Ala Leu Val Ser Met Leu Val Leu Arg Val	375	380	385	
cga gtg agc gat gcg ctg agc gtc ttt ggc gag act tta aaa gaa atg	1256			
Arg Val Ser Asp Ala Leu Ser Val Phe Gly Glu Thr Leu Lys Glu Met	390	395	400	
cgt tac ccc att ctc acc att ggt tta gtc tta agc ttt gcc tat gtg	1304			
Arg Tyr Pro Ile Leu Thr Ile Gly Leu Val Leu Ser Phe Ala Tyr Val	405	410	415	
tct aat tac agc ggg att tct tcc act cta gcc tta gcg ctc acg cat	1352			
Ser Asn Tyr Ser Gly Ile Ser Ser Thr Leu Ala Leu Ala Leu Thr His	420	425	430	
acg ggt ttg gct ttc acc ttt ttc tcg ccc ttg atc ggg tgg gta ggc	1400			
Thr Gly Leu Ala Phe Thr Phe Phe Ser Pro Leu Ile Gly Trp Val Gly	435	440	445	450
gtg ttt tta acc ggg agc gat acg agt tcc aat ctt ttg ttt ggc tct	1448			
Val Phe Leu Thr Gly Ser Asp Thr Ser Ser Asn Leu Leu Phe Gly Ser	455	460	465	
tta cag caa ctc acc gcc caa cga ttg cac ctc cct gag gtt tta acc	1496			
Leu Gln Gln Leu Thr Ala Gln Arg Leu His Leu Pro Glu Val Leu Thr	470	475	480	
cta acg gct aat acc gtg ggt ggc act tta ggc aag atg ata agc cct	1544			
Leu Thr Ala Asn Thr Val Gly Gly Thr Leu Gly Lys Met Ile Ser Pro	485	490	495	
caa agc atc gct atc gct tgc gcg gcg gtg ggg tta gcc ggg aaa gag	1592			
Gln Ser Ile Ala Ile Ala Cys Ala Ala Val Gly Leu Ala Gly Lys Glu	500	505	510	
agc gat ttg ttc aaa ttc acg gtt aaa tac tcc ctt att ttt gta gcg	1640			
Ser Asp Leu Phe Lys Phe Thr Val Lys Tyr Ser Leu Ile Phe Val Ala	515	520	525	530
atc atg gga gtt gtg atc agc gcg att gcg tat ttg atc cct gaa gtg	1688			

Ile Met Gly Val Val Ile Ser Ala Ile Ala Tyr Leu Ile Pro Glu Val
535 540 545

gtg cct gcg ata aag tagggccatt ttagatttag cagggttta cccccaaata 1743
Val Pro Ala Ile Lys
550

aatttttttg ttt 1756

<210> 268
<211> 551
<212> PRT
<213> Helicobacter pylori

<400> 268
Val Leu Glu Phe His Gln Ile Tyr Asp Pro Leu Gly Asn Ile Trp Leu
1 5 10 15
Ser Ala Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu
20 25 30
Met Val Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala
35 40 45
Leu Ser Ala Val Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met
50 55 60
Val Gly Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile
65 70 75 80
Ala Trp Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys
85 90 95
Ser Gly Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu
100 105 110
Asp His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe
115 120 125
Leu Glu Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala
130 135 140
Ile Leu Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys
145 150 155 160
Leu Ile Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro
165 170 175
Ile Ser Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser
180 185 190
Ala Met Thr Gly Lys Ile Leu Phe Phe Val Ser Leu Leu Val Pro Phe
195 200 205
Phe Ile Val Phe Leu Met Asp Gly Phe Lys Gly Ile Lys Glu Thr Phe
210 215 220
Pro Ala Val Phe Ile Ala Ala Phe Ser Phe Ala Gly Ala Gln Phe Leu
225 230 235 240
Ser Ser Asn Tyr Leu Gly Pro Glu Leu Pro Gly Ile Ile Ser Ala Leu
245 250 255
Val Ser Leu Val Ala Thr Ala Leu Phe Leu Lys Phe Trp Gln Pro Lys
260 265 270
Ala Ile Phe Arg Ser Asp Gly Lys Ala Ala Ser Phe Thr Lys Ser Asn
275 280 285
His His Ile Cys Lys Ile Tyr Val Ala Trp Ser Pro Phe Val Ile Leu
290 295 300
Val Leu Val Ile Val Leu Trp Ile Gln Pro Phe Phe Lys Ala Leu Phe
305 310 315 320
Glu Lys Asp Gly Leu Leu Ala Phe Ser Asn Phe Tyr Phe Glu Phe Asn
325 330 335
Asn Ile Ser Asn His Ile Phe Lys Ser Pro Pro Phe Val Glu Ala Asn
340 345 350

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<213> Helicobacter pylori

<400> 270

Met Asp Phe Leu Asn Asp His Ile Asn Val Phe Gly Leu Ile Ala Ala
1 5 10 15
Leu Val Ile Leu Val Leu Thr Ile Tyr Glu Ser Ser Ser Leu Ile Lys
20 25 30
Glu Met Arg Asp Ser Lys Ser Gln Gly Glu Leu Val Glu Asn Gly His
35 40 45
Leu Ile Asp Gly Ile Gly Glu Phe Ala Asn Asn Val Pro Val Gly Trp
50 55 60
Ile Ala Ser Phe Met Cys Thr Ile Val Trp Ala Phe Trp Tyr Phe Phe
65 70 75 80
Phe Gly Tyr Pro Leu Asn Ser Phe Ser Gln Ile Gly Gln Tyr Asn Glu
85 90 95
Glu Val Lys Ala His Asn Gln Lys Phe Glu Ala Lys Trp Lys His Leu
100 105 110
Gly Gln Lys Glu Leu Val Asp Met Gly Gln Gly Ile Phe Leu Val His
115 120 125
Cys Ser Gln Cys His Gly Ile Thr Ala Glu Gly Leu His Gly Ser Ala
130 135 140
Gln Asn Leu Val Arg Trp Gly Lys Glu Glu Gly Ile Met Asp Thr Ile
145 150 155 160
Lys His Gly Ser Lys Gly Met Asp Tyr Leu Ala Gly Glu Met Pro Ala
165 170 175
Met Glu Leu Asp Glu Lys Asp Ala Lys Ala Ile Ala Ser Tyr Val Met
180 185 190
Ala Glu Leu Ser Ser Val Lys Lys Thr Lys Asn Pro Gln Leu Ile Asp
195 200 205
Lys Gly Lys Glu Leu Phe Glu Ser Met Gly Cys Thr Gly Cys His Gly
210 215 220
Asn Asp Gly Lys Gly Leu Gln Glu Asn Gln Val Phe Ala Ala Asp Leu
225 230 235 240
Thr Ala Tyr Gly Thr Glu Asn Phe Leu Arg Asn Ile Leu Thr His Gly
245 250 255
Lys Lys Gly Asn Ile Gly His Met Pro Ser Phe Lys Tyr Lys Asn Phe
260 265 270
Ser Asp Leu Gln Val Lys Ala Leu Leu Asn Leu Ser Asn Arg
275 280 285

<210> 271

<211> 307

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(254)

<400> 271

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Met Lys
1
ttt tta aac gga tta gca ggg aat tta ctg att gtg gtt att tta ttg 104
Phe Leu Asn Gly Leu Ala Gly Asn Leu Leu Ile Val Val Ile Leu Leu
5 10 15
tgt gtg gcc gtt ttt ttt acg ctc aaa gcg atc cat atc caa aaa gag 152

att tta aac gct aaa gcg caa aac atg cct aaa gac aat att gac gca	248
Ile Leu Asn Ala Lys Ala Gln Asn Met Pro Lys Asp Asn Ile Asp Ala	
55 60 65	
gcg att aaa aga gcg agc agt aaa gaa ggg aat ttg agt gaa atc act	296
Ala Ile Lys Arg Ala Ser Ser Lys Glu Gly Asn Leu Ser Glu Ile Thr	
70 75 80	
tat gaa ggt aag gcg aat ttt ggc gtg cta atc atc atg gaa tgc atg	344
Tyr Glu Gly Lys Ala Asn Phe Gly Val Leu Ile Ile Met Glu Cys Met	
85 90 95	
act gat aac ccc acc aga acc att gcc aac ctt aaa agc tat ttc aat	392
Thr Asp Asn Pro Thr Arg Thr Ile Ala Asn Leu Lys Ser Tyr Phe Asn	
100 105 110	
aaa acg caa ggg gca agc atc gtg cct aat ggc tct tta gag ttt atg	440
Lys Thr Gln Gly Ala Ser Ile Val Pro Asn Gly Ser Leu Glu Phe Met	
115 120 125 130	
ttt aac cga aaa agc gtg ttt gaa tgc ttg aaa aat gaa gtg gaa aat	488
Phe Asn Arg Lys Ser Val Phe Glu Cys Leu Lys Asn Glu Val Glu Asn	
135 140 145	
tta aaa ctc agt cta gaa gat tta gaa ttc gct ctc att gat tat ggt	536
Leu Lys Leu Ser Leu Glu Asp Leu Glu Phe Ala Leu Ile Asp Tyr Gly	
150 155 160	
ttg gaa gaa tta gaa gaa gtg gaa gac aag atc att att agg ggg gat	584
Leu Glu Glu Leu Glu Glu Val Glu Asp Lys Ile Ile Arg Gly Asp	
165 170 175	
tat aac agc ttc aag ctt tta aat gag ggg ttt gaa agc ttg aaa tta	632
Tyr Asn Ser Phe Lys Leu Leu Asn Glu Gly Phe Glu Ser Leu Lys Leu	
180 185 190	
ccc att tta aaa gcg agt ttg caa cgc atc gcc aca acg ccc att gaa	680
Pro Ile Leu Lys Ala Ser Leu Gln Arg Ile Ala Thr Thr Pro Ile Glu	
195 200 205 210	
ttg aat gac gaa caa atg gag ctt acc gaa aaa tta ctg gac agg att	728
Leu Asn Asp Glu Gln Met Glu Leu Thr Glu Lys Leu Leu Asp Arg Ile	
215 220 225	
gaa gac gat gat gat gtg gtc gcg ctt tat acc aat att gag	770
Glu Asp Asp Asp Asp Val Val Ala Leu Tyr Thr Asn Ile Glu	
230 235 240	
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aatgcgttgg aga	843

<210> 274

<211> 240

<212> PRT

<213> Helicobacter pylori

<400> 274

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Ala Ala Lys Asp Gly Gly Ser Glu Pro Asp Thr Asn Ala Lys Leu Arg			
35	40	45	
Thr Ala Ile Leu Asn Ala Lys Ala Gln Asn Met Pro Lys Asp Asn Ile			
50	55	60	
Asp Ala Ala Ile Lys Arg Ala Ser Ser Lys Glu Gly Asn Leu Ser Glu			
65	70	75	80
Ile Thr Tyr Glu Gly Lys Ala Asn Phe Gly Val Leu Ile Ile Met Glu			
85	90	95	
Cys Met Thr Asp Asn Pro Thr Arg Thr Ile Ala Asn Leu Lys Ser Tyr			
100	105	110	
Phe Asn Lys Thr Gln Gly Ala Ser Ile Val Pro Asn Gly Ser Leu Glu			
115	120	125	
Phe Met Phe Asn Arg Lys Ser Val Phe Glu Cys Leu Lys Asn Glu Val			
130	135	140	
Glu Asn Leu Lys Leu Ser Leu Glu Asp Leu Glu Phe Ala Leu Ile Asp			
145	150	155	160
Tyr Gly Leu Glu Glu Leu Glu Glu Val Glu Asp Lys Ile Ile Ile Arg			
165	170	175	
Gly Asp Tyr Asn Ser Phe Lys Leu Leu Asn Glu Gly Phe Glu Ser Leu			
180	185	190	
Lys Leu Pro Ile Leu Lys Ala Ser Leu Gln Arg Ile Ala Thr Thr Pro			
195	200	205	
Ile Glu Leu Asn Asp Glu Gln Met Glu Leu Thr Glu Lys Leu Leu Asp			
210	215	220	
Arg Ile Glu Asp Asp Asp Asp Val Val Ala Leu Tyr Thr Asn Ile Glu			
225	230	235	240

<210> 275
 <211> 451
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (108)...(392)

<400> 275	
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aagcgataga atacaacaaa aagggtcagg ggcattttat aggcacc atg gtt gtc	116
Met Val Val	
1	
gct aag aat gaa gac aac aaa aaa ttg tat gac atc att gac ggc cag	164
Ala Lys Asn Glu Asp Asn Lys Lys Leu Tyr Asp Ile Ile Asp Gly Gln	
5 10 15	
caa cga acg act acc atc ttc atg ctc ttg cat gtc ttg gcg aac aaa	212
Gln Arg Thr Thr Thr Ile Phe Met Leu Leu His Val Leu Ala Asn Lys	
20 25 30 35	
caa aac gag aaa gac aag caa gaa aca aga aaa tat cta tac caa aag	260
Gln Asn Glu Lys Asp Lys Gln Glu Thr Arg Lys Tyr Leu Tyr Gln Lys	
40 45 50	
ggg gaa tta aaa tta gaa gtc gcc ccc aaa aac caa agc ttc ttc aaa	308
Gly Glu Leu Lys Leu Glu Val Ala Pro Lys Asn Gln Ser Phe Phe Lys	

<212> PRT
<213> Helicobacter pylori

<400> 280
Met Asp Leu Leu Phe Ala Thr Pro Thr Ile Ser Pro Phe Leu Pro Phe
1 5 10 15
Lys Asn Pro Met Ile Phe Leu Tyr Lys Asn Glu Met Ile Val Leu Lys
20 25 30
Phe Ser Asn Ser Gln Asp Ala Leu Pro Ile Asn Lys Pro Ser Thr Leu
35 40 45
Ser Ile Pro Lys Ile Ser Leu Ala Phe Cys Val Phe Thr Leu Pro Pro
50 55 60
Tyr Asn Lys Gly Val Phe
65 70

<210> 281
<211> 1271
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (368)...(1210)

<400> 281
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gtatccctgc tggcgtgagc ttattttcca tgctagcaaa cgccaaacga gagagagaga 120
gagagagaga gtaaaactct tttatcaaat ccattgtttg gtggagagtt taaccccaga 180
gaatatagcc aaattagaag aaacgatcgc tcctttttaga gctttttcta gcatagagtt 240
tttgatatt accgataaag aattagaacc acgccacaat tataataagc ttgatccttt 300
aatagcgagt gaaattaaaa aattgtattt aaaactcaat gctttttcgc aaaaacgctt 360
ttctaaa atg atc atg tgc cgt ttc ttt ttt gcc tcc ctt ttc ccc caa 409
Met Ile Met Cys Arg Phe Phe Phe Ala Ser Leu Phe Pro Gln
1 5 10
tac gat aag atg atc atg ttt gat gtg gac act ttg ttt gtg aat gat 457
Tyr Asp Lys Met Ile Met Phe Asp Val Asp Thr Leu Phe Val Asn Asp
15 20 25 30
att agc gag agc ttt ttt atc ccc ctt gaa acg cat tat ttt ggg gct 505
Ile Ser Glu Ser Phe Phe Ile Pro Leu Glu Thr His Tyr Phe Gly Ala
35 40 45
gtg agg gaa aaa gat ttg atc gct ata aat agg aat tcg gct aag gat 553
Val Arg Glu Lys Asp Leu Ile Ala Ile Asn Arg Asn Ser Ala Lys Asp
50 55 60
tta tac gaa ttg cgc caa atg cat gca aaa tct atc ggc atc gcc aac 601
Leu Tyr Glu Leu Arg Gln Met His Ala Lys Ser Ile Gly Ile Ala Asn
65 70 75
gct ttc cct aat tta gaa gaa gct caa atc ctt ttt gac aac tac ttt 649
Ala Phe Pro Asn Leu Glu Glu Ala Gln Ile Leu Phe Asp Asn Tyr Phe
80 85 90
aac gcc ggg ttt tta gcc tta aat tta aaa tca tgg cgt aaa gaa aat 697
Asn Ala Gly Phe Leu Ala Leu Asn Leu Lys Ser Trp Arg Lys Glu Asn
95 100 105 110

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355 360 365 370

ata ggg gtt gtg gtg ggg gtt tta gtc aat gcg tta tgg atc aaa tct 1208
 Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile Lys Ser
 375 380 385

aaa ggg att gca tgaaatttta ttttaaaaag ttgggtagct agagatatgg 1260
 Lys Gly Ile Ala
 390

ctccagatgt agg 1273

<210> 286
 <211> 390
 <212> PRT
 <213> Helicobacter pylori

<400> 286

Met	Arg	Lys	Lys	Gly	Met	Phe	Glu	Lys	Ile	Gln	Lys	Glu	Trp	Leu	Ser
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			20					25					30		
Ile	Pro	Glu	Thr	Ala	Gly	Phe	Ala	Ile	Met	Val	Gly	Leu	Asp	Val	Gly
		35					40					45			
Val	Ala	Phe	Tyr	Thr	Thr	Phe	Tyr	Met	Ala	Phe	Val	Leu	Ser	Leu	Phe
	50					55					60				
Gly	Ala	Arg	Lys	Ala	Met	Ile	Ser	Ala	Ala	Ala	Gly	Ser	Val	Ala	Leu
65					70				75					80	
Ile	Leu	Val	Gly	Val	Val	Lys	Asn	Tyr	Gly	Leu	Glu	Tyr	Ala	Gly	Val
				85					90					95	
Ala	Thr	Leu	Met	Ala	Gly	Val	Leu	Gln	Ile	Leu	Leu	Gly	Tyr	Leu	Lys
			100					105					110		
Ile	Gly	Asn	Leu	Leu	Arg	Phe	Ile	Pro	Gln	Ser	Val	Met	Tyr	Gly	Phe
		115					120					125			
Val	Asn	Ala	Leu	Gly	Ile	Leu	Leu	Leu	Met	Glu	Gln	Phe	Lys	Phe	Leu
	130					135					140				
Gln	Asn	Gln	Asn	Leu	Gly	Val	Phe	Val	Leu	Leu	Ala	Ile	Gly	Ile	Leu
145				150					155					160	
Ile	Ile	Tyr	Leu	Phe	Pro	Leu	Ile	Thr	Lys	Lys	Ile	Pro	Ser	Asn	Leu
				165					170					175	
Ile	Cys	Ile	Leu	Ile	Val	Ser	Ala	Ile	Ala	Leu	Ile	Phe	Asp	Met	His
		180						185					190		
Ala	Pro	Asn	Leu	Gly	Ser	Ile	Glu	Gln	Gly	Val	Ser	Gly	Phe	His	Phe
		195					200					205			
Ile	Ile	Ile	Pro	Lys	Asn	Leu	Asp	Phe	Lys	Ile	Met	Ile	Glu	Leu	Leu
	210					215					220				
Pro	Tyr	Ala	Leu	Ser	Leu	Ala	Leu	Val	Gly	Thr	Ile	Glu	Ser	Leu	Leu
225					230					235				240	
Thr	Ala	Lys	Thr	Leu	Asp	Val	Ile	Leu	Lys	Asp	Gly	Val	Ser	Asp	Lys
				245					250					255	
Asn	Lys	Glu	Thr	Lys	Ala	Gln	Gly	Leu	Gly	Asn	Ile	Ile	Ser	Gly	Leu
			260					265					270		
Leu	Gly	Gly	Met	Thr	Gly	Cys	Ala	Leu	Val	Gly	Gln	Ser	Ile	Ile	Asn
		275					280					285			
Ala	Lys	Ser	Gly	Ala	Lys	Thr	Arg	Leu	Ser	Thr	Phe	Phe	Ala	Gly	Phe
	290					295					300				
Ser	Leu	Met	Val	Leu	Ile	Leu	Val	Phe	Asn	Glu	Tyr	Val	Val	Lys	Ile
305					310				315					320	
Pro	Ile	Val	Ala	Val	Val	Ala	Val	Met	Val	Met	Ile	Ser	Phe	Thr	Thr

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Leu Asn Gly Gly Cys Gln Ile Pro Ile Gly Val His Ala Ser Leu Met
125 130 135

ggc gat agg gtt aaa atc cag gcg gtt tta ggc ttg cct aac ggg aaa 844
Gly Asp Arg Val Lys Ile Gln Ala Val Leu Gly Leu Pro Asn Gly Lys
140 145 150

gaa gtc att act aaa gaa aaa caa ggg gat aaa act aaa gcg ttt gat 892
Glu Val Ile Thr Lys Glu Lys Gln Gly Asp Lys Thr Lys Ala Phe Asp
155 160 165

tta gtt caa gag ctt tta gaa gaa ttt ttg caa agc ggg gct aaa gag 940
Leu Val Gln Glu Leu Leu Glu Glu Phe Leu Gln Ser Gly Ala Lys Glu
170 175 180 185

att tta gaa aag gcg cag ttg ttt taatgcgttt gtttatcgcg ctagttttgt 994
Ile Leu Glu Lys Ala Gln Leu Phe
190

tttgggtggtg gttaagcttg aacgct 1020

<210> 288
<211> 193
<212> PRT
<213> Helicobacter pylori

<400> 288

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Ser Met Gln Ile Lys Leu Lys Arg Gln Asp Leu Asp Thr Glu Ser Leu
20 25 30
Arg Gly Asn Val Gln Thr Arg Leu Lys Lys Leu Glu Cys Gly Glu Phe
35 40 45
Asp Ala Ile Ile Leu Ala Glu Ala Gly Leu Cys Arg Leu Glu Ile Gln
50 55 60
Gly Ala Lys Tyr Arg Lys Ala Phe Ser Val Glu Glu Met Ile Pro Ser
65 70 75 80
Met Gly Gln Gly Ala Leu Gly Val Glu Met Leu Lys Asn His Lys His
85 90 95
Phe Ala Thr Leu Gln Lys Leu Asn Asp Glu Lys Ser Ala Phe Cys Cys
100 105 110
Arg Leu Glu Arg Glu Phe Ile Lys Gly Leu Asn Gly Gly Cys Gln Ile
115 120 125
Pro Ile Gly Val His Ala Ser Leu Met Gly Asp Arg Val Lys Ile Gln
130 135 140
Ala Val Leu Gly Leu Pro Asn Gly Lys Glu Val Ile Thr Lys Glu Lys
145 150 155 160
Gln Gly Asp Lys Thr Lys Ala Phe Asp Leu Val Gln Glu Leu Leu Glu
165 170 175
Glu Phe Leu Gln Ser Gly Ala Lys Glu Ile Leu Glu Lys Ala Gln Leu
180 185 190
Phe

<210> 289
<211> 265
<212> DNA
<213> Helicobacter pylori

[illegible]

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Val	Arg	Tyr	Gln	Gly	Gly	His	Asn	Ala	Gly	His	Thr	Ile	Val	His	Lys	
30				35				40				45				
ggg	ggt	aag	cat	tct	ttg	cat	tta	atg	cct	tca	ggg	ggt	tta	tac	ccc	255
Gly	Val	Lys	His	Ser	Leu	His	Leu	Met	Pro	Ser	Gly	Val	Leu	Tyr	Pro	
				50				55				60				
aaa	tgc	aag	aac	atc	att	tct	agc	gcg	gtg	gtc	gtg	agc	ggt	aag	gat	303
Lys	Cys	Lys	Asn	Ile	Ile	Ser	Ser	Ala	Val	Val	Val	Ser	Val	Lys	Asp	
				65				70				75				
ttg	tgc	gaa	gaa	atc	agc	gcg	ttt	gag	gat	tta	gaa	aat	cgt	ttg	ttt	351
Leu	Cys	Glu	Glu	Ile	Ser	Ala	Phe	Glu	Asp	Leu	Glu	Asn	Arg	Leu	Phe	
				80				85				90				
gtc	agc	gac	aga	gcc	cat	gtg	atc	ttg	ccc	tat	cat	gcc	aaa	aaa	gac	399
Val	Ser	Asp	Arg	Ala	His	Val	Ile	Leu	Pro	Tyr	His	Ala	Lys	Lys	Asp	
				95				100				105				
gct	ttt	aaa	gaa	aaa	tct	caa	aac	atc	ggc	acg	act	aaa	aaa	ggc	ata	447
Ala	Phe	Lys	Glu	Lys	Ser	Gln	Asn	Ile	Gly	Thr	Thr	Lys	Lys	Gly	Ile	
110				115				120				125				
ggc	cct	tgc	tat	gag	gat	aaa	atg	gcc	agg	agc	ggg	ata	aga	atg	ggg	495
Gly	Pro	Cys	Tyr	Glu	Asp	Lys	Met	Ala	Arg	Ser	Gly	Ile	Arg	Met	Gly	
				130				135				140				
gat	tta	tta	gac	gat	aaa	atc	tta	gaa	gaa	aag	cta	aac	gct	cat	ttc	543
Asp	Leu	Leu	Asp	Asp	Lys	Ile	Leu	Glu	Glu	Lys	Leu	Asn	Ala	His	Phe	
				145				150				155				
aaa	gcc	att	gag	cct	ttt	aaa	aaa	gcg	tat	gat	ttg	ggc	gag	aat	tac	591
Lys	Ala	Ile	Glu	Pro	Phe	Lys	Lys	Ala	Tyr	Asp	Leu	Gly	Glu	Asn	Tyr	
				160				165				170				
gaa	aaa	gat	ttg	atg	ggg	tat	ttt	aaa	act	tac	gct	cca	aaa	att	tgc	639
Glu	Lys	Asp	Leu	Met	Gly	Tyr	Phe	Lys	Thr	Tyr	Ala	Pro	Lys	Ile	Cys	
				175				180				185				
ccc	ttt	atc	aaa	gac	acg	aca	agc	atg	ctg	ata	gaa	gcg	aat	caa	aag	687
Pro	Phe	Ile	Lys	Asp	Thr	Thr	Ser	Met	Leu	Ile	Glu	Ala	Asn	Gln	Lys	
190				195				200				205				
ggt	gaa	aaa	atc	cta	tta	gaa	ggg	gca	caa	ggc	acg	ctt	tta	gac	att	735
Gly	Glu	Lys	Ile	Leu	Leu	Glu	Gly	Ala	Gln	Gly	Thr	Leu	Leu	Asp	Ile	
				210				215				220				
gat	tta	ggg	act	tac	cct	ttt	gta	aca	agc	tct	aac	acc	acg	agc	gct	783
Asp	Leu	Gly	Thr	Tyr	Pro	Phe	Val	Thr	Ser	Ser	Asn	Thr	Thr	Ser	Ala	
				225				230				235				
agc	gca	tgc	gtg	agc	acc	ggc	tta	aac	cct	aaa	gcg	atc	aat	gaa	gtc	831
Ser	Ala	Cys	Val	Ser	Thr	Gly	Leu	Asn	Pro	Lys	Ala	Ile	Asn	Glu	Val	
				240				245				250				
ata	ggt</															

gcg act ttt ttg caa gtt agg gtt caa ggg gaa gtg agt aat ttg act	152
Ala Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr	
20 25 30	
atc cat aag gtg agc ggc cat gcg tat ttt tcg ctc aaa gac agc cag	200
Ile His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln	
35 40 45 50	
tcg gtt att aaa tgc gtg ctg ttt aaa ggg aac gct aac agg ctc aaa	248
Ser Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys	
55 60 65	
ttc gct tta aaa gaa ggg cag gaa gtg gtt gtt ttt ggg ggt att agc	296
Phe Ala Leu Lys Glu Gly Gln Glu Val Val Phe Gly Gly Ile Ser	
70 75 80	
gtg tat gtc cca agg ggg gat tat caa atc aat tgc ttt gaa ata gag	344
Val Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu	
85 90 95	
cct aag gat ata ggt tca tta act tta gct tta gag caa ttg aaa gaa	392
Pro Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu	
100 105 110	
aaa tta cgc ctt aaa ggc tat ttt gat gaa gaa aat aaa tta ccc aaa	440
Lys Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu Pro Lys	
115 120 125 130	
ccg cat ttt cct aaa cga gtg gca gtc atc act tct caa aat tca gcc	488
Pro His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn Ser Ala	
135 140 145	
gct tgg gcg gac atg aaa aag atc gct tcc aaa cga tgg ccg atg tgt	536
Ala Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro Met Cys	
150 155 160	
gaa tta gtt tgt atc aac acc tta atg caa ggg gag ggc tgc gtt caa	584
Glu Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys Val Gln	
165 170 175	
agc gtg gtg gaa agc atc gtt tat gcg gat agt ttt cat gac aca aaa	632
Ser Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp Thr Lys	
180 185 190	
aac gct ttt gat gcg att gta gtg gct agg ggt ggg ggg agc atg gag	680
Asn Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser Met Glu	
195 200 205 210	
gat ttg tat tct ttc aat gat gaa aaa atc gct gat gct ctg tat ttg	728
Asp Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu Tyr Leu	
215 220 225	
gcc aaa acc ttc agc atg tca gct att ggg cat gag agc gat ttt tta	776
Ala Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp Phe Leu	
230 235 240	
ttg agc gat tta gtg gcg gat tta agg gct tct acg cct tca aac gcg	824
Leu Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser Asn Ala	
245 250 255	

Ser Gln Ser Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg
50 55 60
Leu Lys Phe Ala Leu Lys Glu Gly Gln Glu Val Val Phe Gly Gly
65 70 75 80
Ile Ser Val Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu
85 90 95
Ile Glu Pro Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu
100 105 110
Lys Glu Lys Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu
115 120 125
Pro Lys Pro His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn
130 135 140
Ser Ala Ala Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro
145 150 155 160
Met Cys Glu Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys
165 170 175
Val Gln Ser Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp
180 185 190
Thr Lys Asn Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser
195 200 205
Met Glu Asp Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu
210 215 220
Tyr Leu Ala Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp
225 230 235 240
Phe Leu Leu Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser
245 250 255
Asn Ala Met Glu Ile Leu Leu Pro Ser Ser Asp Glu Trp Leu Gln Arg
260 265 270
Leu Asp Gly Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu
275 280 285
His Gln Lys Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg
290 295 300
Leu Ser Phe Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys
305 310 315 320
Leu Lys Ile Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys
325 330 335
Lys Thr Leu Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe
340 345 350
Leu Gln Thr Lys Thr Glu Arg Leu Asn Arg Leu Glu Asn Ala Leu Lys
355 360 365
Leu Ala His Ala Asn Leu Lys Leu Pro Gln Phe Gly Ala Leu Val Ser
370 375 380
Lys Asn Asn Gln Ala Ile Glu Leu Glu Ala Leu Lys Arg Gly Asp Lys
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Lys Gly Leu Lys Lys Ala Phe Lys Glu Arg Phe Cys Ser Gln Val Tyr		
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Ile Ser Phe Asn Val Asp His Asn Leu Leu Ser Thr Gln Val Ile Arg		
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atc aaa aac gat cgc att aaa gag aaa ttt ttt aaa act ttt gag act		200
Ile Lys Asn Asp Arg Ile Lys Glu Lys Phe Phe Lys Thr Phe Glu Thr		
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aaa gtg gag act aaa aat ggt gaa gtc cct att caa gcc tta aaa atc		248
Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu Lys Ile		
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gcc aga act tat agc caa aaa tac ccc tac act tat ttt agc gcg atg		296
Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser Ala Met		
	70 75 80	
agt aaa gct aaa gag gtt tta tgc gaa aag cag gcg ttt gaa caa atc		344
Ser Lys Ala Lys Glu Val Leu Cys Glu Lys Gln Ala Phe Glu Gln Ile		
	85 90 95	
aaa caa gaa aat caa gat tat cat gct tgt gaa gtc aat caa aag tat		392
Lys Gln Glu Asn Gln Asp Tyr His Ala Cys Glu Val Asn Gln Lys Tyr		
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tgc gtt tat gtg gaa tct aag gat ttt tta aag gat ttt aag cgt ttt		440
Cys Val Tyr Val Glu Ser Lys Asp Phe Leu Lys Asp Phe Lys Arg Phe		
	115 120 125 130	
aaa atc cag gat gtg gat ttt ttg ttt tcg cct ttt agc ctt att tat		488
Lys Ile Gln Asp Val Asp Phe Leu Phe Ser Pro Phe Ser Leu Ile Tyr		
	135 140 145	
gat ttt gtg cgc gat aat tta gaa aat aag ccg ttg ttg tat ttg ctt		536
Asp Phe Val Arg Asp Asn Leu Glu Asn Lys Pro Leu Leu Tyr Leu Leu		
	150 155 160	
ttg gag cgt tca aga ttt tat ttt ttg att gcg gat aaa aaa gag att		584
Leu Glu Arg Ser Arg Phe Tyr Phe Leu Ile Ala Asp Lys Lys Glu Ile		
	165 170 175	
ttt tta gcc aaa tcc gtg ttt tta gaa gaa caa cct gaa gag ttt ata		632
Phe Leu Ala Lys Ser Val Phe Leu Glu Glu Gln Pro Glu Glu Phe Ile		
	180 185 190	
gag agc aaa gaa gaa gat ttt atg gga atg gat aat gag gct gtg gat		680
Glu Ser Lys Glu Glu Asp Phe Met Gly Met Asp Asn Glu Ala Val Asp		
	195 200 205 210	
ttg ttt ttg agt gaa atc caa gaa gat att gac agc ctt gaa gaa gcg		728
Leu Phe Leu Ser Glu Ile Gln Glu Asp Ile Asp Ser Leu Glu Glu Ala		
	215 220 225	

ata ggc cta gac agc agt aag gat aat agc gaa aaa ata aca gag gac	776
Ile Gly Leu Asp Ser Ser Lys Asp Asn Ser Glu Lys Ile Thr Glu Asp	
230 235 240	
gct tat agt ttg att gaa ggc atg acg aat atc ccc tta att gca gat	824
Ala Tyr Ser Leu Ile Glu Gly Met Thr Asn Ile Pro Leu Ile Ala Asp	
245 250 255	
gtt ttg caa gag gga ttg cgt ggc gtc tat cat tct aga gag ata gac	872
Val Leu Gln Glu Gly Leu Arg Gly Val Tyr His Ser Arg Glu Ile Asp	
260 265 270	
ttt gta gaa aaa gtg gtt gtt tta gac agc tgt caa atc cac caa aaa	920
Phe Val Glu Lys Val Val Val Leu Asp Ser Cys Gln Ile His Gln Lys	
275 280 285 290	
gcg tta atg cat ttg caa gaa act ttg atg ata gaa gtg gat agg ctt	968
Ala Leu Met His Leu Gln Glu Thr Leu Met Ile Glu Val Asp Arg Leu	
295 300 305	
gat ttt tct tta gtg gag cgc ttg aac att tta gcg cgc atg gag aat	1016
Asp Phe Ser Leu Val Glu Arg Leu Asn Ile Leu Ala Arg Met Glu Asn	
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ctttctaaaa tt	1083
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Ile Arg Ile Lys Asn Asp Arg Ile Lys Glu Lys Phe Phe Lys Thr Phe	
35 40 45	
Glu Thr Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu	
50 55 60	
Lys Ile Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser	
65 70 75 80	
Ala Met Ser Lys Ala Lys Glu Val Leu Cys Glu Lys Gln Ala Phe Glu	
85 90 95	
Gln Ile Lys Gln Glu Asn Gln Asp Tyr His Ala Cys Glu Val Asn Gln	
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Lys Tyr Cys Val Tyr Val Glu Ser Lys Asp Phe Leu Lys Asp Phe Lys	
115 120 125	
Arg Phe Lys Ile Gln Asp Val Asp Phe Leu Phe Ser Pro Phe Ser Leu	
130 135 140	
Ile Tyr Asp Phe Val Arg Asp Asn Leu Glu Asn Lys Pro Leu Leu Tyr	
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Leu Leu Leu Glu Arg Ser Arg Phe Tyr Phe Leu Ile Ala Asp Lys Lys	
165 170 175	

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Ser Leu Ser Asp Asn Val Lys Leu Gln Glu Asp Gly Ile Val Phe Lys	
100 105 110	
tcc cat att gat ggg agc aag cat cta ttc acg ccc gct aaa gtt ttg	444
Ser His Ile Asp Gly Ser Lys His Leu Phe Thr Pro Ala Lys Val Leu	
115 120 125	
gac att caa tat tct ttg aat agc gat att atg atg gtt tta gac gat	492
Asp Ile Gln Tyr Ser Leu Asn Ser Asp Ile Met Met Val Leu Asp Asp	
130 135 140 145	
tta gtg ggc ttg ccc gct ccc tta aaa cgc ctt gaa gaa tcc att aaa	540
Leu Val Gly Leu Pro Ala Pro Leu Lys Arg Leu Glu Glu Ser Ile Lys	
150 155 160	
aga agt gct aaa tgg gcg aat atg agc cta gaa tac cac aaa gaa aaa	588
Arg Ser Ala Lys Trp Ala Asn Met Ser Leu Glu Tyr His Lys Glu Lys	
165 170 175	
aac cgc ccg agc aac aac ctt ttt gcc att atc cag ggc ggg acg cat	636
Asn Arg Pro Ser Asn Asn Leu Phe Ala Ile Ile Gln Gly Gly Thr His	
180 185 190	
ttg aaa atg cgc agc ctt agc gtg gga tta acg cat gag ggt ttt gat	684
Leu Lys Met Arg Ser Leu Ser Val Gly Leu Thr His Glu Gly Phe Asp	
195 200 205	
ggc tac gct ata ggc ggt tta gcg gtg ggg gaa agc gct gat gaa atg	732
Gly Tyr Ala Ile Gly Gly Leu Ala Val Gly Glu Ser Ala Asp Glu Met	
210 215 220 225	
cta gaa acc atc gcg cac acc gcc ccc ttg ctc ccc aaa gac aag cct	780
Leu Glu Thr Ile Ala His Thr Ala Pro Leu Leu Pro Lys Asp Lys Pro	
230 235 240	
cgc tac tta atg ggc gta ggc acg cct gaa aat atc cta gac gct atc	828
Arg Tyr Leu Met Gly Val Gly Thr Pro Glu Asn Ile Leu Asp Ala Ile	
245 250 255	
agt ttg ggg gtg gat atg ttt gat tgc gtg atg ccc acc aga aac gcc	876
Ser Leu Gly Val Asp Met Phe Asp Cys Val Met Pro Thr Arg Asn Ala	
260 265 270	
aga aac gcc acc ctt ttc acg cat tct ggc aaa att tct atc aaa aac	924
Arg Asn Ala Thr Leu Phe Thr His Ser Gly Lys Ile Ser Ile Lys Asn	
275 280 285	
gcg ccc tat aaa ttg gat aat acc cct att gaa gaa aat tgc gca tgt	972
Ala Pro Tyr Lys Leu Asp Asn Thr Pro Ile Glu Glu Asn Cys Ala Cys	
290 295 300 305	
tat gct tgc aaa cgc tat tct aaa gcc tat ttg cac cat tta ttt agg	1020
Tyr Ala Cys Lys Arg Tyr Ser Lys Ala Tyr Leu His His Leu Phe Arg	
310 315 320	
gct aaa gaa ctc act tac gct cgt ttg gcc agc ttg cac aat ttg cat	1068
Ala Lys Glu Leu Thr Tyr Ala Arg Leu Ala Ser Leu His Asn Leu His	
325 330 335	

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Phe Tyr Leu Glu Leu Val Lys Asn Ala Arg Asn Ala Ile Leu Glu Lys
340 345 350

cgg ttt ttg agt ttt aaa aaa gaa ttt ttg gag aaa tac aac tcc cgc 1164
Arg Phe Leu Ser Phe Lys Lys Glu Phe Leu Glu Lys Tyr Asn Ser Arg
355 360 365

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Ser His
370

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35 40 45
Ile Leu Gly Ala Lys Leu Ile Leu Ala Asn Thr Tyr His Met Tyr Leu
50 55 60
Arg Pro Gly Glu Lys Val Val Glu Glu Leu Gly Gly Leu His Arg Phe
65 70 75 80
Ala Gln Phe Tyr Gly Ser Phe Leu Thr Asp Ser Gly Gly Phe Gln Ala
85 90 95
Phe Ser Leu Ser Asp Asn Val Lys Leu Gln Glu Asp Gly Ile Val Phe
100 105 110
Lys Ser His Ile Asp Gly Ser Lys His Leu Phe Thr Pro Ala Lys Val
115 120 125
Leu Asp Ile Gln Tyr Ser Leu Asn Ser Asp Ile Met Met Val Leu Asp
130 135 140
Asp Leu Val Gly Leu Pro Ala Pro Leu Lys Arg Leu Glu Glu Ser Ile
145 150 155 160
Lys Arg Ser Ala Lys Trp Ala Asn Met Ser Leu Glu Tyr His Lys Glu
165 170 175
Lys Asn Arg Pro Ser Asn Asn Leu Phe Ala Ile Ile Gln Gly Gly Thr
180 185 190
His Leu Lys Met Arg Ser Leu Ser Val Gly Leu Thr His Glu Gly Phe
195 200 205
Asp Gly Tyr Ala Ile Gly Gly Leu Ala Val Gly Glu Ser Ala Asp Glu
210 215 220
Met Leu Glu Thr Ile Ala His Thr Ala Pro Leu Leu Pro Lys Asp Lys
225 230 235 240
Pro Arg Tyr Leu Met Gly Val Gly Thr Pro Glu Asn Ile Leu Asp Ala
245 250 255
Ile Ser Leu Gly Val Asp Met Phe Asp Cys Val Met Pro Thr Arg Asn
260 265 270
Ala Arg Asn Ala Thr Leu Phe Thr His Ser Gly Lys Ile Ser Ile Lys
275 280 285
Asn Ala Pro Tyr Lys Leu Asp Asn Thr Pro Ile Glu Glu Asn Cys Ala
290 295 300

0989591-062904

Cys Tyr Ala Cys Lys Arg Tyr Ser Lys Ala Tyr Leu His His Leu Phe
 305 310 315 320
 Arg Ala Lys Glu Leu Thr Tyr Ala Arg Leu Ala Ser Leu His Asn Leu
 325 330 335
 His Phe Tyr Leu Glu Leu Val Lys Asn Ala Arg Asn Ala Ile Leu Glu
 340 345 350
 Lys Arg Phe Leu Ser Phe Lys Lys Glu Phe Leu Glu Lys Tyr Asn Ser
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 Arg Ser His
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 Lys Val Tyr Phe Lys Thr Phe Gly Cys Arg Thr Asn Leu Phe Asp Thr
 5 10 15
 caa gtg atg agc gag aat ttg aag gac ttt agc acg acc tta gaa gaa 152
 Gln Val Met Ser Glu Asn Leu Lys Asp Phe Ser Thr Thr Leu Glu Glu
 20 25 30
 caa gaa gcc gat att att atc atc aat tct tgc acc gtg acc aat ggg 200
 Gln Glu Ala Asp Ile Ile Ile Ile Asn Ser Cys Thr Val Thr Asn Gly
 35 40 45 50
 gcc gat agc gcg gta agg agt tac gct aaa aaa atg gca cgg ttg gat 248
 Ala Asp Ser Ala Val Arg Ser Tyr Ala Lys Lys Met Ala Arg Leu Asp
 55 60 65
 aag gaa gtg cta ttt act ggt tgc ggg gtg aaa acc caa ggc aaa gag 296
 Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly Lys Glu
 70 75 80
 ctt ttt gaa aaa ggg ttt tta aag ggc gtt ttt ggg cat gac aat aaa 344
 Leu Phe Glu Lys Gly Phe Leu Lys Gly Val Phe Gly His Asp Asn Lys
 85 90 95
 gaa aag att aac gcg ctt tta caa gaa aaa aag cgt ttt ttt ata gat 392
 Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe Ile Asp
 100 105 110
 gac aat tta gaa aac aag cac tta gac acc acg atg gtg agc gag ttt 440
 Asp Asn Leu Glu Asn Lys His Leu Asp Thr Thr Met Val Ser Glu Phe
 115 120 125 130
 gtg gga aaa act agg gcg ttt att aag atc caa gaa ggc tgt gat ttt 488
 Val Gly Lys Thr Arg Ala Phe Ile Lys Ile Gln Glu Gly Cys Asp Phe

106290-ET656860

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	Asp Cys Asn Tyr Cys Ile Ile Pro Ser Val Arg Gly Arg Ala Arg Ser			
	150	155	160	
	ttt gaa gag aga aaa att tta gag caa gtg ggc ctt tta tgc tct aaa			584
	Phe Glu Glu Arg Lys Ile Leu Glu Gln Val Gly Leu Leu Cys Ser Lys			
	165	170	175	
	ggg gtt caa gaa gtg gtt tta acc ggc acc aat gtg ggg agc tat ggg			632
	Gly Val Gln Glu Val Val Leu Thr Gly Thr Asn Val Gly Ser Tyr Gly			
	180	185	190	
	aaa gat aga gga agc aat atc gcg cga ttg att aaa aaa tta agc cag			680
	Lys Asp Arg Gly Ser Asn Ile Ala Arg Leu Ile Lys Lys Leu Ser Gln			
	195	200	205	210
	atc gct gga tta aaa cgc ata agg att ggg agc tta gaa cct aat caa			728
	Ile Ala Gly Leu Lys Arg Ile Arg Ile Gly Ser Leu Glu Pro Asn Gln			
	215	220	225	
	att aac gat gaa ttt tta gag ctt tta gaa gag gat ttt tta gaa aaa			776
	Ile Asn Asp Glu Phe Leu Glu Leu Leu Glu Glu Asp Phe Leu Glu Lys			
	230	235	240	
	cat ttg cat atc gct tta cag cac agc cat gat ctc atg cta gag agg			824
	His Leu His Ile Ala Leu Gln His Ser His Asp Leu Met Leu Glu Arg			
	245	250	255	
	atg aat cga aga aac cgc act aaa agc gat agg gaa tta tta gaa aca			872
	Met Asn Arg Arg Asn Arg Thr Lys Ser Asp Arg Glu Leu Leu Glu Thr			
	260	265	270	
	atc gct tct aag aat ttt gct att ggc acg gat ttt att gtg ggg cat			920
	Ile Ala Ser Lys Asn Phe Ala Ile Gly Thr Asp Phe Ile Val Gly His			
	275	280	285	290
	ccg ggc gag agc gga agc gtt ttt gaa aaa gcg ttt aaa aat tta gaa			968
	Pro Gly Glu Ser Gly Ser Val Phe Glu Lys Ala Phe Lys Asn Leu Glu			
	295	300	305	
	agc ttg cct tta acg cac atc cac cct ttt att tac agc aaa cga aaa			1016
	Ser Leu Pro Leu Thr His Ile His Pro Phe Ile Tyr Ser Lys Arg Lys			
	310	315	320	
	gac acc ccc tct agc ttg atg act gat agc gtg agt ttg gaa gat tct			1064
	Asp Thr Pro Ser Ser Leu Met Thr Asp Ser Val Ser Leu Glu Asp Ser			
	325	330	335	
	aaa aag cgt ttg aat gcg att aaa gat ttg att ttt cat aaa aat aag			1112
	Lys Lys Arg Leu Asn Ala Ile Lys Asp Leu Ile Phe His Lys Asn Lys			
	340	345	350	
	gcg ttc agg caa ttg cag ctc aag ctc aat acg cct cta aaa gcc tta			1160
	Ala Phe Arg Gln Leu Gln Leu Lys Leu Asn Thr Pro Leu Lys Ala Leu			
	355	360	365	370
	gtg gaa gtg caa aaa gac ggc gaa ttt aaa gcc tta gat caa ttt ttc			1208

Val Glu Val Gln Lys Asp Gly Glu Phe Lys Ala Leu Asp Gln Phe Phe
375 380 385

aac ccc att aaa atc aaa agc gat aag cct cta agg gct agt ttt tta 1256
Asn Pro Ile Lys Ile Lys Ser Asp Lys Pro Leu Arg Ala Ser Phe Leu
390 395 400

gaa atc aaa gag tat gaa att aag gag agg gaa aat cat gcc gtt ttc 1304
Glu Ile Lys Glu Tyr Glu Ile Lys Glu Arg Glu Asn His Ala Val Phe
405 410 415

taaaaattta gaaaatctta ccgctccctt caaacgcatt aaaaaccgct cgc 1357

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<213> Helicobacter pylori

<400> 300

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Asn Gly Ala Asp Ser Ala Val Arg Ser Tyr Ala Lys Lys Met Ala Arg
50 55 60
Leu Asp Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly
65 70 75 80
Lys Glu Leu Phe Glu Lys Gly Phe Leu Lys Gly Val Phe Gly His Asp
85 90 95
Asn Lys Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe
100 105 110
Ile Asp Asp Asn Leu Glu Asn Lys His Leu Asp Thr Thr Met Val Ser
115 120 125
Glu Phe Val Gly Lys Thr Arg Ala Phe Ile Lys Ile Gln Glu Gly Cys
130 135 140
Asp Phe Asp Cys Asn Tyr Cys Ile Ile Pro Ser Val Arg Gly Arg Ala
145 150 155 160
Arg Ser Phe Glu Glu Arg Lys Ile Leu Glu Gln Val Gly Leu Leu Cys
165 170 175
Ser Lys Gly Val Gln Glu Val Val Leu Thr Gly Thr Asn Val Gly Ser
180 185 190
Tyr Gly Lys Asp Arg Gly Ser Asn Ile Ala Arg Leu Ile Lys Lys Leu
195 200 205
Ser Gln Ile Ala Gly Leu Lys Arg Ile Arg Ile Gly Ser Leu Glu Pro
210 215 220
Asn Gln Ile Asn Asp Glu Phe Leu Glu Leu Leu Glu Glu Asp Phe Leu
225 230 235 240
Glu Lys His Leu His Ile Ala Leu Gln His Ser His Asp Leu Met Leu
245 250 255
Glu Arg Met Asn Arg Arg Asn Arg Thr Lys Ser Asp Arg Glu Leu Leu
260 265 270
Glu Thr Ile Ala Ser Lys Asn Phe Ala Ile Gly Thr Asp Phe Ile Val
275 280 285
Gly His Pro Gly Glu Ser Gly Ser Val Phe Glu Lys Ala Phe Lys Asn
290 295 300
Leu Glu Ser Leu Pro Leu Thr His Ile His Pro Phe Ile Tyr Ser Lys
305 310 315 320

106290-ET65860

Lys	Thr	Ser	Leu	Phe	Glu	Ile	Phe	Lys	Ala	Leu	Phe	Pro	Cys	Gly	Ser	
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Val	Thr	Gly	Cys	Pro	Lys	Ile	Lys	Thr	Met	Gln	Ile	Ile	Glu	Ser	Leu	
275					280					285					290	
gaa	aaa	cgc	cct	agg	ggg	gtg	tat	tgc	ggg	gcg	ata	ggc	atg	gtt	gaa	968
Glu	Lys	Arg	Pro	Arg	Gly	Val	Tyr	Cys	Gly	Ala	Ile	Gly	Met	Val	Glu	
				295					300					305		
gaa	aaa	aaa	gcc	ctt	ttt	agc	gtg	cct	atc	cgc	act	tta	gaa	aaa	aga	1016
Glu	Lys	Lys	Ala	Leu	Phe	Ser	Val	Pro	Ile	Arg	Thr	Leu	Glu	Lys	Arg	
			310					315					320			
gtg	cac	gaa	aat	ttt	ttg	cat	tta	ggg	gta	ggg	agt	ggg	gta	act	tat	1064
Val	His	Glu	Asn	Phe	Leu	His	Leu	Gly	Val	Gly	Ser	Gly	Val	Thr	Tyr	
		325					330					335				
aaa	agt	aaa	gcg	cca	aaa	gaa	tat	gaa	gaa	agc	ttt	ttg	aaa	tcc	ttt	1112
Lys	Ser	Lys	Ala	Pro	Lys	Glu	Tyr	Glu	Glu	Ser	Phe	Leu	Lys	Ser	Phe	
	340					345					350					
ttt	gtg	atg	ccc	aaa	ata	gaa	ttt	gag	att	gta	gaa	acg	atg	aaa	att	1160
Phe	Val	Met	Pro	Lys	Ile	Glu	Phe	Glu	Ile	Val	Glu	Thr	Met	Lys	Ile	
355					360					365					370	
atc	aaa	aag	gat	caa	aaa	tta	gag	att	aat	aat	aaa	aac	gcc	cat	aaa	1208
Ile	Lys	Lys	Asp	Gln	Lys	Leu	Glu	Ile	Asn	Asn	Lys	Asn	Ala	His	Lys	
				375					380					385		
gaa	cgc	tta	atg	aat	agc	act	cga	tat	ttt	aac	ttt	aaa	tac	gat	gaa	1256
Glu	Arg	Leu	Met	Asn	Ser	Thr	Arg	Tyr	Phe	Asn	Phe	Lys	Tyr	Asp	Glu	
			390					395					400			
aat	ctt	tta	gat	ttt	gaa	tta	gaa	aaa	gaa	ggg	gtt	tta	agg	gtt	tta	1304
Asn	Leu	Leu	Asp	Phe	Glu	Leu	Glu	Lys	Glu	Gly	Val	Leu	Arg	Val	Leu	
		405					410					415				
ctc	aat	aaa	aag	ggc	aag	ctc	att	aaa	gaa	tac	aaa	acc	tta	gag	cct	1352
Leu	Asn	Lys	Lys	Gly	Lys	Leu	Ile	Lys	Glu	Tyr	Lys	Thr	Leu	Glu	Pro	
	420					425					430					
tta	aaa	agc	cta	gaa	atc	cgt	ttg	agt	gaa	gcc	ccc	att	gat	aaa	cgc	1400
Leu	Lys	Ser	Leu	Glu	Ile	Arg	Leu	Ser	Glu	Ala	Pro	Ile	Asp	Lys	Arg	
435					440					445					450	
aat	gat	ttt	tta	tac	cat	aag	acc	act	tat	gcc	cct	ttt	tat	caa	aag	1448
Asn	Asp	Phe	Leu	Tyr	His	Lys	Thr	Thr	Tyr	Ala	Pro	Phe	Tyr	Gln	Lys	
				455					460					465		
gct	cga	gcg	ctc	att	aaa	aag	ggc	gtt	atg	ttt	gat	gaa	atc	ttt	tat	1496
Ala	Arg	Ala	Leu	Ile	Lys	Lys	Gly	Val	Met	Phe	Asp	Glu	Ile			

275	280	285
Ser Leu Glu Lys Arg Pro	Arg Gly Val Tyr Cys Gly	Ala Ile Gly Met
290	295	300
Val Glu Glu Lys Lys Ala	Leu Phe Ser Val Pro	Ile Arg Thr Leu Glu
305	310	315
Lys Arg Val His Glu Asn	Phe Leu His Leu Gly	Val Gly Ser Gly Val
325	330	335
Thr Tyr Lys Ser Lys Ala	Pro Lys Glu Tyr Glu	Glu Ser Phe Leu Lys
340	345	350
Ser Phe Phe Val Met Pro	Lys Ile Glu Phe Glu	Ile Val Glu Thr Met
355	360	365
Lys Ile Ile Lys Lys Asp	Gln Lys Leu Glu Ile	Asn Asn Lys Asn Ala
370	375	380
His Lys Glu Arg Leu Met	Asn Ser Thr Arg Tyr	Phe Asn Phe Lys Tyr
385	390	395
Asp Glu Asn Leu Leu Asp	Phe Glu Leu Glu Lys	Glu Gly Val Leu Arg
405	410	415
Val Leu Leu Asn Lys Lys	Gly Lys Leu Ile Lys	Glu Tyr Lys Thr Leu
420	425	430
Glu Pro Leu Lys Ser Leu	Glu Ile Arg Leu Ser	Glu Ala Pro Ile Asp
435	440	445
Lys Arg Asn Asp Phe Leu	Tyr His Lys Thr Thr	Tyr Ala Pro Phe Tyr
450	455	460
Gln Lys Ala Arg Ala Leu	Ile Lys Lys Gly Val	Met Phe Asp Glu Ile
465	470	475
Phe Tyr Asn Gln Asp Leu	Glu Leu Thr Glu Gly	Ala Arg Ser Asn Leu
485	490	495
Val Leu Glu Ile His Asn	Arg Leu Leu Thr Pro	Tyr Phe Ser Ala Gly
500	505	510
Ala Leu Asn Gly Thr Gly	Val Val Gly Leu Leu	Lys Lys Gly Leu Val
515	520	525
Gly His Ala Pro Leu Lys	Leu Gln Asp Leu Gln	Lys Ala Ser Lys Ile
530	535	540
Tyr Cys Ile Asn Ala Leu	Tyr Gly Leu Val Glu	Val Lys Ile Lys
545	550	555

<210> 305
 <211> 958
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(905)

<400> 305	
ttagtgata ttttatacgc ttttattgat cctagaataa ggttggtcata atg gag	56
Met Glu	
1	
tct ttt aga gag ttt atc caa caa ttc aaa aaa aat aag gca gcg gtc	104
Ser Phe Arg Glu Phe Ile Gln Gln Phe Lys Lys Asn Lys Ala Ala Val	
5 10 15	
ggt ggg gct tgg att gtg ctt tta ttg gta att tgc gcg att ttt gcg	152
Val Gly Ala Trp Ile Val Leu Leu Val Ile Cys Ala Ile Phe Ala	
20 25 30	
ccc ctt tta gcc ccg cat gat cct tat gtc caa aac gcg caa gat cgc	200

Pro 35	Leu	Leu	Ala	Pro	His 40	Asp	Pro	Tyr	Val	Gln 45	Asn	Ala	Gln	Asp	Arg 50	
ctt	ttg	aag	cct	ata	tgg	gag	cat	gga	ggg	aat	gct	aaa	tac	ctt	tta	248
Leu	Leu	Lys	Pro	Ile 55	Trp	Glu	His	Gly	Gly 60	Asn	Ala	Lys	Tyr	Leu 65	Leu	
ggc	acc	gat	gat	ttg	ggg	cgc	gat	att	ttg	agc	cgc	ttg	atc	tat	ggg	296
Gly	Thr	Asp	Asp 70	Leu	Gly	Arg	Asp	Ile 75	Leu	Ser	Arg	Leu	Ile 80	Tyr	Gly	
gcc	agg	att	tct	tta	acc	ata	ggg	att	gtt	tct	atg	ggg	att	gcg	gtg	344
Ala	Arg	Ile 85	Ser	Leu	Thr	Ile	Gly 90	Ile	Val	Ser	Met	Gly 95	Ile	Ala	Val	
ttt	ttt	ggc	acg	ata	cta	ggg	cta	ata	gcg	ggg	tat	ttt	ggg	ggg	aaa	392
Phe	Phe 100	Gly	Thr	Ile	Leu	Gly 105	Leu	Ile	Ala	Gly	Tyr 110	Phe	Gly	Gly	Lys	
aca	gat	gca	att	atc	atg	cgt	atc	atg	gac	atc	atg	ttc	gct	ttg	ccc	440
Thr	Asp	Ala	Ile	Ile	Met 120	Arg	Ile	Met	Asp	Ile 125	Met	Phe	Ala	Leu	Pro 130	
tct	att	tta	ttg	atc	gtg	att	gtg	gtc	gcg	gtg	tta	ggg	cct	tca	ctc	488
Ser	Ile	Leu	Leu 135	Ile	Val	Ile	Val	Val	Ala 140	Val	Leu	Gly	Pro	Ser 145	Leu	
act	aac	gcc	atg	ctc	gct	att	ggg	ttt	gtg	ggg	att	cct	ggg	ttt	gca	536
Thr	Asn	Ala 150	Met	Leu	Ala	Ile	Gly	Phe 155	Val	Gly	Ile	Pro	Gly 160	Phe	Ala	
aga	ttg	gtg	cgc	agt	tcc	gtg	cta	ggg	gaa	aaa	gaa	aaa	gaa	tac	gtg	584
Arg	Leu 165	Val	Arg	Ser	Ser	Val	Leu 170	Gly	Glu	Lys	Glu	Lys 175	Glu	Tyr	Val	
atc	gct	tct	aaa	atc	aat	ggc	tct	tcg	cat	ctt	cggt	ttg	atg	tgt	aag	632
Ile	Ala 180	Ser	Lys	Ile	Asn	Gly 185	Ser	Ser	His	Leu	Arg	Leu	Met	Cys	Lys	
gtg	att	ttc	cct	aat	tgc	att	atc	cct	tta	atc	gtt	caa	acg	aca	atg	680
Val	Ile 195	Phe	Pro	Asn	Cys 200	Ile	Ile	Pro	Leu	Ile 205	Val	Gln	Thr	Thr 210	Met	
ggg	ttt	gct	tcc	acg	gtt	tta	gaa	gcg	gct	gca	ctg	agc	ttc	tta	ggg	728
Gly	Phe	Ala	Ser 215	Thr	Val	Leu	Glu	Ala	Ala 220	Ala	Leu	Ser	Phe	Leu 225	Gly	
ctt	ggg	gcc	caa	cct	ccc	aaa	ccc	gaa	tgg	gga	gcg	atg	ttg	atg	aat	776
Leu	Gly	Ala 230	Gln	Pro	Pro	Lys	Pro	Glu 235	Trp	Gly	Ala	Met	Leu 240	Met	Asn	
tcc	atg	caa	tac	atc	gct	acc	gct	cct	tgg	atg	ctt	gtt	ttc	cct	ggg	824
Ser	Met	Gln 245	Tyr	Ile	Ala	Thr	Ala 250	Pro	Trp	Met	Leu	Val 255	Phe	Pro	Gly	
gtg	atg	att	ttt	tta	acg	gtc	atg	agt	ttt	aat	ctg	gta	ggc	gat	ggc	872
Val	Met 260	Ile	Phe	Leu	Thr 265	Val	Met	Ser	Phe	Asn	Leu 270	Val	Gly	Asp	Gly	

atc atg gac gct tta gat cct aaa cgc acc tct taaaaggagc ttgcatgatt 925
 Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser
 275 280 285

ttagaagtta aagatttaaa aacttatttt ttc 958

<210> 306
 <211> 285
 <212> PRT
 <213> Helicobacter pylori

<400> 306
 Met Glu Ser Phe Arg Glu Phe Ile Gln Gln Phe Lys Lys Asn Lys Ala
 1 5 10 15
 Ala Val Val Gly Ala Trp Ile Val Leu Leu Val Ile Cys Ala Ile
 20 25 30
 Phe Ala Pro Leu Leu Ala Pro His Asp Pro Tyr Val Gln Asn Ala Gln
 35 40 45
 Asp Arg Leu Leu Lys Pro Ile Trp Glu His Gly Gly Asn Ala Lys Tyr
 50 55 60
 Leu Leu Gly Thr Asp Asp Leu Gly Arg Asp Ile Leu Ser Arg Leu Ile
 65 70 75 80
 Tyr Gly Ala Arg Ile Ser Leu Thr Ile Gly Ile Val Ser Met Gly Ile
 85 90 95
 Ala Val Phe Phe Gly Thr Ile Leu Gly Leu Ile Ala Gly Tyr Phe Gly
 100 105 110
 Gly Lys Thr Asp Ala Ile Ile Met Arg Ile Met Asp Ile Met Phe Ala
 115 120 125
 Leu Pro Ser Ile Leu Leu Ile Val Ile Val Ala Val Leu Gly Pro
 130 135 140
 Ser Leu Thr Asn Ala Met Leu Ala Ile Gly Phe Val Gly Ile Pro Gly
 145 150 155 160
 Phe Ala Arg Leu Val Arg Ser Ser Val Leu Gly Glu Lys Glu Lys Glu
 165 170 175
 Tyr Val Ile Ala Ser Lys Ile Asn Gly Ser Ser His Leu Arg Leu Met
 180 185 190
 Cys Lys Val Ile Phe Pro Asn Cys Ile Ile Pro Leu Ile Val Gln Thr
 195 200 205
 Thr Met Gly Phe Ala Ser Thr Val Leu Glu Ala Ala Leu Ser Phe
 210 215 220
 Leu Gly Leu Gly Ala Gln Pro Pro Lys Pro Glu Trp Gly Ala Met Leu
 225 230 235 240
 Met Asn Ser Met Gln Tyr Ile Ala Thr Ala Pro Trp Met Leu Val Phe
 245 250 255
 Pro Gly Val Met Ile Phe Leu Thr Val Met Ser Phe Asn Leu Val Gly
 260 265 270
 Asp Gly Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser
 275 280 285

<210> 307
 <211> 791
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (95)...(727)

<400> 307

00665913-0665901

0985913 "062901"

ccttggttaaa aatgtagt ggtgcaagct tgctgacaca cgccttaata gctaaagaag	60
aaagcgcagc ncttcttgga caaaaaatgt gtat atg gga gtc aat tac caa aca	115
Met Gly Val Asn Tyr Gln Thr	
1 5	
ggt tct atc aat tta atg act aat atc cat gaa gtt aga gaa gtt act	163
Gly Ser Ile Asn Leu Met Thr Asn Ile His Glu Val Arg Glu Val Thr	
10 15 20	
aac tat caa acc ggt tac acc aat att ata act agc gtt aat agc gtt	211
Asn Tyr Gln Thr Gly Tyr Thr Asn Ile Ile Thr Ser Val Asn Ser Val	
25 30 35	
aaa aag ctc acc aac atg gga tct aat ggg att gga tta gtc atg ggt	259
Lys Lys Leu Thr Asn Met Gly Ser Asn Gly Ile Gly Leu Val Met Gly	
40 45 50 55	
tat aac cac ttt ttc cat ccg gat aaa atc ttg ggc ttg cgc tat ttc	307
Tyr Asn His Phe Phe His Pro Asp Lys Ile Leu Gly Leu Arg Tyr Phe	
60 65 70	
gct ttt tta gat tgg caa ggc tat ggc atg aga tac cct aaa ggc tat	355
Ala Phe Leu Asp Trp Gln Gly Tyr Gly Met Arg Tyr Pro Lys Gly Tyr	
75 80 85	
tat ggc ggc aat aac atg atc act tat ggc gtg ggc gtg gat gca gtg	403
Tyr Gly Gly Asn Asn Met Ile Thr Tyr Gly Val Gly Val Asp Ala Val	
90 95 100	
tgg aat ttc ttt caa ggg agt ttc tat caa gat gac att agc gtg gat	451
Trp Asn Phe Phe Gln Gly Ser Phe Tyr Gln Asp Asp Ile Ser Val Asp	
105 110 115	
att ggc gtt ttt ggg ggg att gcg att gcg ggg aat agc tgg tat att	499
Ile Gly Val Phe Gly Gly Ile Ala Ile Ala Gly Asn Ser Trp Tyr Ile	
120 125 130 135	
ggc agt aaa ggg cag gaa ttg tta ggt atc act aac agc agc gcg gtt	547
Gly Ser Lys Gly Gln Glu Leu Leu Gly Ile Thr Asn Ser Ser Ala Val	
140 145 150	
gat aac acc tct ttt caa ttc ctc ttt aac ttt ggc ctc aag gct tta	595
Asp Asn Thr Ser Phe Gln Phe Leu Phe Asn Phe Gly Leu Lys Ala Leu	
155 160 165	
ttt gta gat gag cat gaa ttt gaa atc ggt ttt aaa ttc ccc acc att	643
Phe Val Asp Glu His Glu Phe Glu Ile Gly Phe Lys Phe Pro Thr Ile	
170 175 180	
aat aac aaa tac tac acc act gac gcg ctc aag gtt caa atg cgt agg	691
Asn Asn Lys Tyr Tyr Thr Thr Asp Ala Leu Lys Val Gln Met Arg Arg	
185 190 195	
gtc ttt gcc ttt tat gtg ggg tat aat tac cac ttc taaagggctt	737
Val Phe Ala Phe Tyr Val Gly Tyr Asn Tyr His Phe	
200 205 210	
ttaaaaccca acgcaactcc ctaacatctt ttggtaatag ctcttggctt tgag	791

<210> 308
 <211> 211
 <212> PRT
 <213> Helicobacter pylori

<400> 308
 Met Gly Val Asn Tyr Gln Thr Gly Ser Ile Asn Leu Met Thr Asn Ile
 1 5 10 15
 His Glu Val Arg Glu Val Thr Asn Tyr Gln Thr Gly Tyr Thr Asn Ile
 20 25 30
 Ile Thr Ser Val Asn Ser Val Lys Lys Leu Thr Asn Met Gly Ser Asn
 35 40 45
 Gly Ile Gly Leu Val Met Gly Tyr Asn His Phe Phe His Pro Asp Lys
 50 55 60
 Ile Leu Gly Leu Arg Tyr Phe Ala Phe Leu Asp Trp Gln Gly Tyr Gly
 65 70 75 80
 Met Arg Tyr Pro Lys Gly Tyr Tyr Gly Gly Asn Asn Met Ile Thr Tyr
 85 90 95
 Gly Val Gly Val Asp Ala Val Trp Asn Phe Phe Gln Gly Ser Phe Tyr
 100 105 110
 Gln Asp Asp Ile Ser Val Asp Ile Gly Val Phe Gly Gly Ile Ala Ile
 115 120 125
 Ala Gly Asn Ser Trp Tyr Ile Gly Ser Lys Gly Gln Glu Leu Leu Gly
 130 135 140
 Ile Thr Asn Ser Ser Ala Val Asp Asn Thr Ser Phe Gln Phe Leu Phe
 145 150 155 160
 Asn Phe Gly Leu Lys Ala Leu Phe Val Asp Glu His Glu Phe Glu Ile
 165 170 175
 Gly Phe Lys Phe Pro Thr Ile Asn Asn Lys Tyr Tyr Thr Thr Asp Ala
 180 185 190
 Leu Lys Val Gln Met Arg Arg Val Phe Ala Phe Tyr Val Gly Tyr Asn
 195 200 205
 Tyr His Phe
 210

<210> 309
 <211> 517
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(464)

<400> 309
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 Met Val
 1
 ggg ggt gga acg gta aaa aaa gac ttg aag aaa gcc att caa tac tat 104
 Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln Tyr Tyr
 5 10 15
 gtt aaa gcg tgt gaa ttg aat gaa atg ttt ggg tgt ctg tca tta gtt 152
 Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser Leu Val
 20 25 30
 tcg aac tct caa ata aac aaa caa aaa ctc ttt caa tat ctc tct aaa 200
 Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu Ser Lys

090909Z FEB 68 : 000000Z

gtggaacgct ctgtcttagc aaattgatct tagcggcgtc gtttttgata gtg gat 56
Val Asp
1

acg att ggc tat ggc tat aat ttg agc gtt tat tct tat gag ggt aag 152
Thr Ile Gly Tyr Gly Tyr Asn Leu Ser Val Tyr Ser Tyr Glu Gly Lys
20 25 30

tgg tat aaa aat ttg gac gca atg agg aga atg gtc atc ttg gat ttg 248
 Trp Tyr Lys Asn Leu Asp Ala Met Arg Arg Met Val Ile Leu Asp Leu
 55 60 65

aag gcc ata gag gat aaa aat tat gct ttg gct gtg gag aga ctg caa 344
Lys Ala Ile Glu Asp Lys Asn Tyr Ala Leu Ala Val Glu Arg Leu Gln
85 90 95

aaa agc ccg tat ttc aat caa gtg aaa aaa gag cgt caa gga ata tgg 392
Lys Ser Pro Tyr Phe Asn Gln Val Lys Lys Glu Arg Gln Gly Ile Trp
100 105 110

aaa ttt tgaaattgga ggggttgcgaa aaacattgta agaaaaaata cgcaatagaa 448
Lys Phe
115

aag 451

	<400>			312											
Val	Asp	Ser	Glu	Gly	Phe	Ser	Pro	Ser	Ile	Tyr	Thr	Asp	Lys	Thr	Gly
1				5					10					15	
His	Pro	Thr	Ile	Gly	Tyr	Gly	Tyr	Asn	Leu	Ser	Val	Tyr	Ser	Tyr	Glu
			20					25					30		
Gly	Lys	Arg	Ile	Thr	Lys	Thr	Tyr	Gly	Leu	Leu	Thr	Asp	Ile	Leu	Ser
		35					40					45			
Tyr	Gly	Trp	Tyr	Lys	Asn	Leu	Asp	Ala	Met	Arg	Arg	Met	Val	Ile	Leu
	50					55					60				
Asp	Leu	Ser	Tyr	Asn	Leu	Gly	Leu	Asn	Gly	Leu	Leu	Lys	Phe	Lys	Gln
65				70						75					80
Phe	Ile	Lys	Ala	Ile	Glu	Asp	Lys	Asn	Tyr	Ala	Leu	Ala	Val	Glu	Arg

0905913 062901

Leu Gln Lys Ser Pro Tyr Phe Asn Gln Val Lys Lys Glu Arg Gln Gly
 100 105 110
 Ile Trp Lys Phe
 115

<210> 313
 <211> 399
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (50)...(346)

<400> 313
 acacaacccat agcgacacaaa aacccgacag acccgccaag gagcgataa aac cca caa 58
 Asn Pro Gln
 1

agc ttt ttc agg aat acg cca cat ttt ttg atc agc cga att ttt atc 106
 Ser Phe Phe Arg Asn Thr Pro His Phe Leu Ile Ser Arg Ile Phe Ile
 5 10 15

cac cag cat gag aat aaa aat cag aat att gac tat gag caa cca aac 154
 His Gln His Glu Asn Lys Asn Gln Asn Ile Asp Tyr Glu Gln Pro Asn
 20 25 30 35

gat aga agc aaa ttc cac gct cac cct ttc aag agc gtt tta aca acc 202
 Asp Arg Ser Lys Phe His Ala His Pro Phe Lys Ser Val Leu Thr Thr
 40 45 50

caa acg cta cca ctt ggt ttt tta gag aga gaa aga gag aga aag caa 250
 Gln Thr Leu Pro Leu Gly Phe Leu Glu Arg Glu Arg Glu Arg Lys Gln
 55 60 65

aat ttt aag att gat tct caa atc tat tcc ttt gca aaa gtt aag att 298
 Asn Phe Lys Ile Asp Ser Gln Ile Tyr Ser Phe Ala Lys Val Lys Ile
 70 75 80

ggg tgt ttt aac atg att ttt ggc ctg ctc gca tca agc cct tat ttt 346
 Gly Cys Phe Asn Met Ile Phe Gly Leu Leu Ala Ser Ser Pro Tyr Phe
 85 90 95

taacatttcc gctcccttgc ttttttaaag cctccctaaa ttactacacc act 399

<210> 314
 <211> 99
 <212> PRT
 <213> Helicobacter pylori

<400> 314
 Asn Pro Gln Ser Phe Phe Arg Asn Thr Pro His Phe Leu Ile Ser Arg
 1 5 10 15
 Ile Phe Ile His Gln His Glu Asn Lys Asn Gln Asn Ile Asp Tyr Glu
 20 25 30
 Gln Pro Asn Asp Arg Ser Lys Phe His Ala His Pro Phe Lys Ser Val
 35 40 45
 Leu Thr Thr Gln Thr Leu Pro Leu Gly Phe Leu Glu Arg Glu Arg Glu

<210> 316
 <211> 140
 <212> PRT
 <213> Helicobacter pylori

<400> 316
 Met Ser Tyr Phe Phe Lys Ile Ile Leu Gly Thr Ser Val Ile Val Gly
 1 5 10 15
 Val Leu Leu Gly Leu Trp Arg Leu Thr Tyr Asp Lys Phe Tyr Phe Ser
 20 25 30
 Leu Val Phe Val Leu Leu Ile Leu Gly Ile Val Ala Cys Ser Tyr Ile
 35 40 45
 Ser Leu Lys Met His Gln Arg Lys Cys Phe Ala Lys Cys Phe Val Asn
 50 55 60
 Ser Glu Ser Phe Leu Ser Lys Met Leu His Ser Pro Ile Met Val Ile
 65 70 75 80
 Cys Phe Tyr Phe Ile Phe Ser Ile Phe Thr Ser Ile Ser Ile Val Tyr
 85 90 95
 Ser Val Leu Asp Tyr Asp Gln Met Met Trp Gly Phe Val Phe Cys Thr
 100 105 110
 Ile Val Val Cys Ala Val Val Phe Gly Thr Leu Glu Lys Asn Ala Gln
 115 120 125
 Glu Tyr His Gln Arg Arg Leu Phe Asp Ala Asp Val
 130 135 140

<210> 317
 <211> 976
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(923)

<400> 317
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 Lys Asn
 1
 cgt agg cgt aac cgc ggc gat gct agc ggc aca gga tta gac aaa ctc 104
 Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp Lys Leu
 5 10 15
 att gac gct tan cct ttg cgc ttt ttt gat gtc gct atc gct gag caa 152
 Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala Glu Gln
 20 25 30
 cac gct tta act tct agc agc gct atg gct aaa gag ggg ttt aaa cct 200
 His Ala Leu Thr Ser Ser Ser Ala Met Ala Lys Glu Gly Phe Lys Pro
 35 40 45 50
 ttt gtg agc atc tat tct act ttt ttg cag agg gct tat gat tct att 248
 Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Ser Ile
 55 60 65
 gtg cat gac gct tgt att tct agc ttg ccg att aaa tta gcc att gac 296
 Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala Ile Asp
 70 75 80

agg gct ggg att gtg ggc gaa gat ggc gag acg cac caa ggg ctt tta	344
Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly Leu Leu	
85 90 95	
gac gtg tcg tat ttg cgc tct atc cct aac atg gtc att ttt gcc cca	392
Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe Ala Pro	
100 105 110	
cga gac aat gag act tta aaa aac gcc gtg cgt ttt gcc aat gaa cac	440
Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn Glu His	
115 120 125 130	
gat tca agc cct tgc gcg ttc cga tac cct agg ggg tcg ttt gcg tta	488
Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe Ala Leu	
135 140 145	
aaa gag ggg gtt ttt gag cct agc ggt ttt gtt tta ggc caa agc gaa	536
Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln Ser Glu	
150 155 160	
ttg ttg aaa aaa gag ggc gaa att tta ctc ata ggc tat ggt aat ggc	584
Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly Asn Gly	
165 170 175	
gtg ggg cgg gcg cat tta gtc caa ctg gct tta aaa gaa aaa aac ata	632
Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys Asn Ile	
180 185 190	
gaa tgc gct ctc ttg gat ctc agg ttt tta aag cct tta gat cca aat	680
Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp Pro Asn	
195 200 205 210	
tta agc gcg atc gtt gcc cct tat caa aag ctc tat gtt ttt agc gat	728
Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe Ser Asp	
215 220 225	
aat tac aag ctt gga ggg gtg gct agc gcg att tta gag ttt ttg agc	776
Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe Leu Ser	
230 235 240	
gaa caa aat att tta aag cct gtt aaa agc ttt gaa atc att gat gaa	824
Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile Asp Glu	
245 250 255	
ttt atc atg cat ggg aac acc gct tta gtg gaa aaa tcc tta gga tta	872
Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu Gly Leu	
260 265 270	
gac aca gag agt ttg act gac gct att tta aaa gat tta gga caa gag	920
Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly Gln Glu	
275 280 285 290	
aga tgaaaaacaaa agcgccaatg aaaaatatcc gcaatttttc cattatcgct	973
cac	976

<210> 318
 <211> 291
 <212> PRT
 <213> Helicobacter pylori

0995913-062901

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<400> 318
Lys Asn Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp
 1          5          10          15
Lys Leu Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala
 20          25          30
Glu Gln His Ala Leu Thr Ser Ser Ala Met Ala Lys Glu Gly Phe
 35          40          45
Lys Pro Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp
 50          55          60
Ser Ile Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala
 65          70          75          80
Ile Asp Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly
 85          90          95
Leu Leu Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe
100          105          110
Ala Pro Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn
115          120          125
Glu His Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe
130          135          140
Ala Leu Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln
145          150          155          160
Ser Glu Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly
165          170          175
Asn Gly Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys
180          185          190
Asn Ile Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp
195          200          205
Pro Asn Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe
210          215          220
Ser Asp Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe
225          230          235          240
Leu Ser Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile
245          250          255
Asp Glu Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu
260          265          270
Gly Leu Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly
275          280          285
Gln Glu Arg
290

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<210> 319
<211> 1135
<212> DNA
<213> Helicobacter pylori

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<220>
<221> CDS
<222> (51)...(1082)

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<400> 319
ggattaagat gttataatag ttgttatttt ttcatttttaa aaggggtttt atg gca      56
                                     Met Ala
                                     1

tta tta ttc aca gga gcg tgc ggg tat ata ggc tcg cat acc gca agg      104
Leu Leu Phe Thr Gly Ala Cys Gly Tyr Ile Gly Ser His Thr Ala Arg
 5          10          15

gcg ttt tta gaa aaa acc aaa gaa aat atc att att gta gat gac tta      152

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09895913 062901

Ala	Phe	Leu	Glu	Lys	Thr	Lys	Glu	Asn	Ile	Ile	Ile	Val	Asp	Asp	Leu	
20						25					30					
agc	acc	ggg	ttt	tta	gag	cac	ctc	aaa	gcg	tta	gag	cat	tat	tac	cct	200
Ser	Thr	Gly	Phe	Leu	Glu	His	Leu	Lys	Ala	Leu	Glu	His	Tyr	Tyr	Pro	
35					40					45					50	
aat	agg	gtt	gtg	ttt	att	caa	gcg	aat	ttg	aat	gaa	acg	cac	aaa	tta	248
Asn	Arg	Val	Val	Phe	Ile	Gln	Ala	Asn	Leu	Asn	Glu	Thr	His	Lys	Leu	
				55					60					65		
gac	gcc	ttt	ttg	aat	aag	cag	cag	cta	aaa	gat	ccc	att	gaa	gcc	atc	296
Asp	Ala	Phe	Leu	Asn	Lys	Gln	Gln	Leu	Lys	Asp	Pro	Ile	Glu	Ala	Ile	
			70					75					80			
ttg	cac	ttt	ggg	gct	aaa	atc	tca	gta	gaa	gaa	tcc	acg	cac	ttg	cct	344
Leu	His	Phe	Gly	Ala	Lys	Ile	Ser	Val	Glu	Glu	Ser	Thr	His	Leu	Pro	
		85					90					95				
tta	gaa	tac	tac	acc	aac	aac	acg	ctc	aac	act	tta	gag	ctt	gtc	aaa	392
Leu	Glu	Tyr	Tyr	Thr	Asn	Asn	Thr	Leu	Asn	Thr	Leu	Glu	Leu	Val	Lys	
100						105					110					
ctt	tgc	tta	aaa	cat	gca	atc	aag	cgt	ttt	att	ttt	tct	tct	acg	gcc	440
Leu	Cys	Leu	Lys	His	Ala	Ile	Lys	Arg	Phe	Ile	Phe	Ser	Ser	Thr	Ala	
115					120					125					130	
gtg	gtt	tat	ggc	gaa	tct	agt	tca	agt	ttg	aat	gaa	gaa	agc	ccc	tta	488
Val	Val	Tyr	Gly	Glu	Ser	Ser	Ser	Ser	Leu	Asn	Glu	Glu	Ser	Pro	Leu	
			135						140					145		
aac	ccc	att	aat	cct	tat	gga	gcg	tct	aaa	atg	atg	agc	gaa	aga	atc	536
Asn	Pro	Ile	Asn	Pro	Tyr	Gly	Ala	Ser	Lys	Met	Met	Ser	Glu	Arg	Ile	
			150					155					160			
ttg	tta	gac	act	tct	aaa	ata	gcg	gat	ttt	aaa	tgc	gtt	att	ttg	cgc	584
Leu	Leu	Asp	Thr	Ser	Lys	Ile	Ala	Asp	Phe	Lys	Cys	Val	Ile	Leu	Arg	
		165					170					175				
tat	ttc	aat	gtg	gct	ggg	gca	tgc	atg	cac	aat	gat	tat	acc	acc	cct	632
Tyr	Phe	Asn	Val	Ala	Gly	Ala	Cys	Met	His	Asn	Asp	Tyr	Thr	Thr	Pro	
	180					185					190					
tac	acg	cta	ggg	caa	cgc	acg	ctc	aac	gcc	acg	cat	ttg	atc	aaa	atc	680
Tyr	Thr	Leu	Gly	Gln	Arg	Thr	Leu	Asn	Ala	Thr	His	Leu	Ile	Lys	Ile	
195					200					205					210	
gca	tgc	gaa	tgc	gcg	gtg	ggg	aaa	agg	aaa	aaa	atg	ggg	att	ttt	ggc	728
Ala	Cys	Glu	Cys	Ala	Val	Gly	Lys	Arg	Lys	Lys	Met	Gly	Ile	Phe	Gly	
				215					220					225		
act	aac	tac	ccc	aca	aga	gat	ggc	act	tgc	att	agg	gat	tat	atc	cat	776
Thr	Asn	Tyr	Pro	Thr	Arg	Asp	Gly	Thr	Cys	Ile	Arg	Asp	Tyr	Ile	His	
			230					235					240			
gta	gat	gat	ttg	gct	aac	gca	cat	tta	gcg	agc	tat	caa	acc	ctt	tta	824
Val	Asp	Asp	Leu	Ala	Asn	Ala	His	Leu	Ala	Ser	Tyr	Gln	Thr	Leu	Leu	
		245					250						255			

gaa aaa aat aag agc gag atc tat aat gtc ggc tac aat caa ggc cat 872
 Glu Lys Asn Lys Ser Glu Ile Tyr Asn Val Gly Tyr Asn Gln Gly His
 260 265 270

agc gtg aaa gaa gtg ata gaa aag gtc aaa gaa atc tca aac aac gat 920
 Ser Val Lys Glu Val Ile Glu Lys Val Lys Glu Ile Ser Asn Asn Asp
 275 280 285 290

ttt tta gtg gaa att tta gac aaa cga cag ggc gat cca gca agc ctt 968
 Phe Leu Val Glu Ile Leu Asp Lys Arg Gln Gly Asp Pro Ala Ser Leu
 295 300 305

att gcc aat aac gct aaa atc tta caa aac acc tct ttc aaa ccc ctt 1016
 Ile Ala Asn Asn Ala Lys Ile Leu Gln Asn Thr Ser Phe Lys Pro Leu
 310 315 320

tat aac aac cta gac acc att atc aaa agc gct cta gat tgg gaa gaa 1064
 Tyr Asn Asn Leu Asp Thr Ile Ile Lys Ser Ala Leu Asp Trp Glu Glu
 325 330 335

cac ctt ttg agg ttt caa taatacaccc tgtgcaaata caagccatta 1112
 His Leu Leu Arg Phe Gln
 340

gccattatgg gcgttcttat agt 1135

<210> 320
 <211> 344
 <212> PRT
 <213> Helicobacter pylori

<400> 320
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 20 25 30
 Asp Leu Ser Thr Gly Phe Leu Glu His Leu Lys Ala Leu Glu His Tyr
 35 40 45
 Tyr Pro Asn Arg Val Val Phe Ile Gln Ala Asn Leu Asn Glu Thr His
 50 55 60
 Lys Leu Asp Ala Phe Leu Asn Lys Gln Gln Leu Lys Asp Pro Ile Glu
 65 70 75 80
 Ala Ile Leu His Phe Gly Ala Lys Ile Ser Val Glu Glu Ser Thr His
 85 90 95
 Leu Pro Leu Glu Tyr Tyr Thr Asn Asn Thr Leu Asn Thr Leu Glu Leu
 100 105 110
 Val Lys Leu Cys Leu Lys His Ala Ile Lys Arg Phe Ile Phe Ser Ser
 115 120 125
 Thr Ala Val Val Tyr Gly Glu Ser Ser Ser Ser Leu Asn Glu Glu Ser
 130 135 140
 Pro Leu Asn Pro Ile Asn Pro Tyr Gly Ala Ser Lys Met Met Ser Glu
 145 150 155 160
 Arg Ile Leu Leu Asp Thr Ser Lys Ile Ala Asp Phe Lys Cys Val Ile
 165 170 175
 Leu Arg Tyr Phe Asn Val Ala Gly Ala Cys Met His Asn Asp Tyr Thr
 180 185 190
 Thr Pro Tyr Thr Leu Gly Gln Arg Thr Leu Asn Ala Thr His Leu Ile
 195 200 205
 Lys Ile Ala Cys Glu Cys Ala Val Gly Lys Arg Lys Lys Met Gly Ile

210		215		220
Phe Gly Thr Asn Tyr	Pro Thr Arg Asp Gly Thr Cys Ile Arg Asp Tyr			
225	230	235	240	
Ile His Val Asp	Leu Ala Asn Ala His Leu Ala Ser Tyr Gln Thr			
	245	250	255	
Leu Leu Glu Lys Asn Lys Ser Glu Ile Tyr Asn Val Gly Tyr Asn Gln				
	260	265	270	
Gly His Ser Val Lys Glu Val Ile Glu Lys Val Lys Glu Ile Ser Asn				
	275	280	285	
Asn Asp Phe Leu Val Glu Ile Leu Asp Lys Arg Gln Gly Asp Pro Ala				
	290	295	300	
Ser Leu Ile Ala Asn Asn Ala Lys Ile Leu Gln Asn Thr Ser Phe Lys				
305	310	315	320	
Pro Leu Tyr Asn Asn Leu Asp Thr Ile Ile Lys Ser Ala Leu Asp Trp				
	325	330	335	
Glu Glu His Leu Leu Arg Phe Gln				
	340			

<210> 321
 <211> 1170
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (97)...(1119)

<400> 321	
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atcattgaga tagttttaag gaaattaagg aacaaa atg gaa gtt tca cgc aag	114
	Met Glu Val Ser Arg Lys
	1 5
aaa att tac aac ccc aat tct aca gaa agt gtg aat gaa aga aag att	162
Lys Ile Tyr Asn Pro Asn Ser Thr Glu Ser Val Asn Glu Arg Lys Ile	
	10 15 20
ttt ggg ggc aat cct aca agc atg ttt gat ttg aat aag atc aag tat	210
Phe Gly Gly Asn Pro Thr Ser Met Phe Asp Leu Asn Lys Ile Lys Tyr	
	25 30 35
caa tgg gcg gat cat ttg tgg aaa acg atg ctc gct aac acc tgg ttt	258
Gln Trp Ala Asp His Leu Trp Lys Thr Met Leu Ala Asn Thr Trp Phe	
	40 45 50
gct gaa gaa gtg agc atg aat gat gac aaa agg gat tat ttg aaa tta	306
Ala Glu Glu Val Ser Met Asn Asp Asp Lys Arg Asp Tyr Leu Lys Leu	
	55 60 65 70
agc gca gag gaa aag atc ggt tat gac aga gct tta gcg caa ctc att	354
Ser Ala Glu Glu Lys Ile Gly Tyr Asp Arg Ala Leu Ala Gln Leu Ile	
	75 80 85
ttt atg gac agc ttg caa gcg aat aat tta att gac aat atc aat ccc	402
Phe Met Asp Ser Leu Gln Ala Asn Asn Leu Ile Asp Asn Ile Asn Pro	
	90 95 100
ttc atc acc agc ccc gaa atc aat ttg tgt ttg gtg cgt caa gct tat	450
Phe Ile Thr Ser Pro Glu Ile Asn Leu Cys Leu Val Arg Gln Ala Tyr	

006290.062901

105	110	115	
gaa gaa gcc cta cac agc cat gcg tat gcg gtg atg gta gaa agc ata Glu Glu Ala Leu His Ser His Ala Tyr Ala Val Met Val Glu Ser Ile 120 125 130			498
agt gcg aat act gaa gag att tat gac atg tgg cgt aac gat atg caa Ser Ala Asn Thr Glu Glu Ile Tyr Asp Met Trp Arg Asn Asp Met Gln 135 140 145 150			546
tta aaa agc aag aac gac tat atc gcg caa gtg tat atg gaa tta gcc Leu Lys Ser Lys Asn Asp Tyr Ile Ala Gln Val Tyr Met Glu Leu Ala 155 160 165			594
aaa aac ccc aca gaa gaa aac att ctc aaa gcg ctt ttt gct aac cag Lys Asn Pro Thr Glu Glu Asn Ile Leu Lys Ala Leu Phe Ala Asn Gln 170 175 180			642
att tta gag ggg att tat ttt tat agc ggg ttt agc tat ttt tac act Ile Leu Glu Gly Ile Tyr Phe Tyr Ser Gly Phe Ser Tyr Phe Tyr Thr 185 190 195			690
ttg gct agg agc ggt aaa atg cta gga tgc gca caa atg att cgt ttt Leu Ala Arg Ser Gly Lys Met Leu Gly Ser Ala Gln Met Ile Arg Phe 200 205 210			738
atc caa aga gat gag gta acg cat ttg att ttg ttc caa aac atg atc Ile Gln Arg Asp Glu Val Thr His Leu Ile Leu Phe Gln Asn Met Ile 215 220 225 230			786
aac gct tta agg aat gaa aga gcg gat ctc ttc acg ccg caa ttg att Asn Ala Leu Arg Asn Glu Arg Ala Asp Leu Phe Thr Pro Gln Leu Ile 235 240 245			834
aat gaa gtc ata gga atg ttt aaa aaa gcg gta gaa att gaa gct ttg Asn Glu Val Ile Gly Met Phe Lys Lys Ala Val Glu Ile Glu Ala Leu 250 255 260			882
tgg ggg gat tat atc acg caa ggc aag att tta ggg ctc act tca agc Trp Gly Asp Tyr Ile Thr Gln Gly Lys Ile Leu Gly Leu Thr Ser Ser 265 270 275			930
ttg att gag caa tac atc cag ttt tta gcg gat agc cgt ttg agt aag Leu Ile Glu Gln Tyr Ile Gln Phe Leu Ala Asp Ser Arg Leu Ser Lys 280 285 290			978
gtg ggc atc gct aaa gtt tat ggc gtc caa cac ccc att aaa tgg gta Val Gly Ile Ala Lys Val Tyr Gly Val Gln His Pro Ile Lys Trp Val 295 300 305 310			1026
gag agc ttt tca agt ttc aat gag cag cgc tct aat ttc ttt gag gct Glu Ser Phe Ser Ser Phe Asn Glu Gln Arg Ser Asn Phe Phe Glu Ala 315 320 325			1074
agg gtg agc aat tac gct aaa ggg agc gtg agt ttt gat gat ttt Arg Val Ser Asn Tyr Ala Lys Gly Ser Val Ser Phe Asp Asp Phe 330 335 340			1119
taaggggctt gtttgaatag tattaataaac catttaaatgt gtgaagaaat c			1170

<210> 322
 <211> 341
 <212> PRT
 <213> Helicobacter pylori

<400> 322
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 Val Asn Glu Arg Lys Ile Phe Gly Gly Asn Pro Thr Ser Met Phe Asp
 20 25 30
 Leu Asn Lys Ile Lys Tyr Gln Trp Ala Asp His Leu Trp Lys Thr Met
 35 40 45
 Leu Ala Asn Thr Trp Phe Ala Glu Glu Val Ser Met Asn Asp Asp Lys
 50 55 60
 Arg Asp Tyr Leu Lys Leu Ser Ala Glu Glu Lys Ile Gly Tyr Asp Arg
 65 70 75 80
 Ala Leu Ala Gln Leu Ile Phe Met Asp Ser Leu Gln Ala Asn Asn Leu
 85 90 95
 Ile Asp Asn Ile Asn Pro Phe Ile Thr Ser Pro Glu Ile Asn Leu Cys
 100 105 110
 Leu Val Arg Gln Ala Tyr Glu Glu Ala Leu His Ser His Ala Tyr Ala
 115 120 125
 Val Met Val Glu Ser Ile Ser Ala Asn Thr Glu Glu Ile Tyr Asp Met
 130 135 140
 Trp Arg Asn Asp Met Gln Leu Lys Ser Lys Asn Asp Tyr Ile Ala Gln
 145 150 155 160
 Val Tyr Met Glu Leu Ala Lys Asn Pro Thr Glu Glu Asn Ile Leu Lys
 165 170 175
 Ala Leu Phe Ala Asn Gln Ile Leu Glu Gly Ile Tyr Phe Tyr Ser Gly
 180 185 190
 Phe Ser Tyr Phe Tyr Thr Leu Ala Arg Ser Gly Lys Met Leu Gly Ser
 195 200 205
 Ala Gln Met Ile Arg Phe Ile Gln Arg Asp Glu Val Thr His Leu Ile
 210 215 220
 Leu Phe Gln Asn Met Ile Asn Ala Leu Arg Asn Glu Arg Ala Asp Leu
 225 230 235 240
 Phe Thr Pro Gln Leu Ile Asn Glu Val Ile Gly Met Phe Lys Lys Ala
 245 250 255
 Val Glu Ile Glu Ala Leu Trp Gly Asp Tyr Ile Thr Gln Gly Lys Ile
 260 265 270
 Leu Gly Leu Thr Ser Ser Leu Ile Glu Gln Tyr Ile Gln Phe Leu Ala
 275 280 285
 Asp Ser Arg Leu Ser Lys Val Gly Ile Ala Lys Val Tyr Gly Val Gln
 290 295 300
 His Pro Ile Lys Trp Val Glu Ser Phe Ser Ser Phe Asn Glu Gln Arg
 305 310 315 320
 Ser Asn Phe Phe Glu Ala Arg Val Ser Asn Tyr Ala Lys Gly Ser Val
 325 330 335
 Ser Phe Asp Asp Phe
 340

<210> 323
 <211> 689
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (139)...(627)

096991.0656360

<400> 323
 caaaagctca ttgaagaaac cccggcagtg gttttagaag agggcggtgcg tgacgtttgc 60
 tagaaacagc gatcaaggcc gctaaatata tcggctrrtg tggggggcggg gactttttgaa 120
 tttttgttg attctaac atg aaa gat ttt tat ttc atg gag atg aac act 171
 Met Lys Asp Phe Tyr Phe Met Glu Met Asn Thr
 1 5 10

cgt ttg caa gtg gaa cac acc att agc gaa atg gtg agc ggg tta aac 219
 Arg Leu Gln Val Glu His Thr Ile Ser Glu Met Val Ser Gly Leu Asn
 15 20 25

ctc att gag tgg atg att aaa atc gct caa ggc gaa aaa ttg ccc aag 267
 Leu Ile Glu Trp Met Ile Lys Ile Ala Gln Gly Glu Lys Leu Pro Lys
 30 35 40

caa gaa agc ttt tct ctc aaa ggc cat gcg ata gaa tgc cga atc acg 315
 Gln Glu Ser Phe Ser Leu Lys Gly His Ala Ile Glu Cys Arg Ile Thr
 45 50 55

gca gaa gat cct aaa aaa ttc tac cca agc ccg ggc aaa att acc gaa 363
 Ala Glu Asp Pro Lys Lys Phe Tyr Pro Ser Pro Gly Lys Ile Thr Glu
 60 65 70 75

tgg atc gct cct ggt ggg gtg aat gtg cgc ctt gat tcg cac gcg cat 411
 Trp Ile Ala Pro Gly Gly Val Asn Val Arg Leu Asp Ser His Ala His
 80 85 90

gcc aat tat gtc gtg cct acg cac tat gat tcg atg att ggc aag ctc 459
 Ala Asn Tyr Val Val Pro Thr His Tyr Asp Ser Met Ile Gly Lys Leu
 95 100 105

att gtg tgg ggt gaa aac aga gaa aga gcg atc gct aag atg aaa agg 507
 Ile Val Trp Gly Glu Asn Arg Glu Arg Ala Ile Ala Lys Met Lys Arg
 110 115 120

gct tta aag gaa ttt aaa gta gaa ggc att aaa acg acc att cct ttc 555
 Ala Leu Lys Glu Phe Lys Val Glu Gly Ile Lys Thr Thr Ile Pro Phe
 125 130 135

cac ctt gaa atg ctt gaa aat gcg gat ttc agg caa gca aaa atc cac 603
 His Leu Glu Met Leu Glu Asn Ala Asp Phe Arg Gln Ala Lys Ile His
 140 145 150 155

acg aag tat tta gaa gaa aat ttt taagttttta ggattctttt aagcatagtt 657
 Thr Lys Tyr Leu Glu Glu Asn Phe
 160

taagggtttt aagcgatcag aaaaagtcag ca 689

<210> 324
 <211> 163
 <212> PRT
 <213> Helicobacter pylori

<400> 324
 Met Lys Asp Phe Tyr Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu
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 His Thr Ile Ser Glu Met Val Ser Gly Leu Asn Leu Ile Glu Trp Met
 20 25 30

Ile Lys Ile Ala Gln Gly Glu Lys Leu Pro Lys Gln Glu Ser Phe Ser
 35 40 45
 Leu Lys Gly His Ala Ile Glu Cys Arg Ile Thr Ala Glu Asp Pro Lys
 50 55 60
 Lys Phe Tyr Pro Ser Pro Gly Lys Ile Thr Glu Trp Ile Ala Pro Gly
 65 70 75 80
 Gly Val Asn Val Arg Leu Asp Ser His Ala His Ala Asn Tyr Val Val
 85 90 95
 Pro Thr His Tyr Asp Ser Met Ile Gly Lys Leu Ile Val Trp Gly Glu
 100 105 110
 Asn Arg Glu Arg Ala Ile Ala Lys Met Lys Arg Ala Leu Lys Glu Phe
 115 120 125
 Lys Val Glu Gly Ile Lys Thr Thr Ile Pro Phe His Leu Glu Met Leu
 130 135 140
 Glu Asn Ala Asp Phe Arg Gln Ala Lys Ile His Thr Lys Tyr Leu Glu
 145 150 155 160
 Glu Asn Phe

<210> 325
 <211> 1960
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1907)

<400> 325
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 Met Phe
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 tat cac tta atc gct cct tta aaa aat aaa acc ccc cct tta acc tat 104
 Tyr His Leu Ile Ala Pro Leu Lys Asn Lys Thr Pro Pro Leu Thr Tyr
 5 10 15
 ttt tct aaa gag caa cac caa aaa gga gcg tta gtc aat atc cct tta 152
 Phe Ser Lys Glu Gln His Gln Lys Gly Ala Leu Val Asn Ile Pro Leu
 20 25 30
 agg aat aaa acg ctt tta ggc gtc gtc ctt gaa gaa gtt tca aaa ccc 200
 Arg Asn Lys Thr Leu Leu Gly Val Val Leu Glu Glu Val Ser Lys Pro
 35 40 45 50
 tct ttt gaa tgc cta gag cta gaa aaa acc cct tat ttt tta ctc ccc 248
 Ser Phe Glu Cys Leu Glu Leu Glu Lys Thr Pro Tyr Phe Leu Leu Pro
 55 60 65
 ttt caa atg gag ctc gct att ttt atc gct caa tat tac tca gct aat 296
 Phe Gln Met Glu Leu Ala Ile Phe Ile Ala Gln Tyr Tyr Ser Ala Asn
 70 75 80
 ctt tct tca gtt tta agc ctt ttt gcc cct ttt aaa gaa tgc gat tta 344
 Leu Ser Ser Val Leu Ser Leu Phe Ala Pro Phe Lys Glu Cys Asp Leu
 85 90 95
 gtg ggg tta gaa aaa att gag cct att ctt aat ata tta agc caa acg 392
 Val Gly Leu Glu Lys Ile Glu Pro Ile Leu Asn Ile Leu Ser Gln Thr

100	105	110	
caa aca aac gct tta aaa gaa ttg caa aaa cat tca gca agc ttg ctc Gln Thr Asn Ala Leu Lys Glu Leu Gln Lys His Ser Ala Ser Leu Leu 115 120 125 130			440
ttt ggc gat acg ggt agc ggg aaa acc gag att tat atg cat gca atc Phe Gly Asp Thr Gly Ser Gly Lys Thr Glu Ile Tyr Met His Ala Ile 135 140 145			488
gcc caa act tta gag caa aaa aaa agc gct tta ttg ttg gtg cca gaa Ala Gln Thr Leu Glu Gln Lys Lys Ser Ala Leu Leu Leu Val Pro Glu 150 155 160			536
atc gct ctc acc cct caa atg caa caa cgc ctt aaa agg gtt ttt aaa Ile Ala Leu Thr Pro Gln Met Gln Gln Arg Leu Lys Arg Val Phe Lys 165 170 175			584
gaa aat tta ggc ttg tgg cat agc aaa ctc tct caa aat caa aaa aaa Glu Asn Leu Gly Leu Trp His Ser Lys Leu Ser Gln Asn Gln Lys Lys 180 185 190			632
caa ttt tta gaa aag ctt tat tcg caa gaa atc aaa tta gtg gta ggc Gln Phe Leu Glu Lys Leu Tyr Ser Gln Glu Ile Lys Leu Val Val Val Gly 195 200 205 210			680
aca cga agc gcg ttg ttt tta ccc ctt aaa gag ctg ggt tta atc att Thr Arg Ser Ala Leu Phe Leu Pro Leu Lys Glu Leu Gly Leu Ile Ile 215 220 225			728
gta gat gaa gag cat gac ttt tct tat aaa tcc cat caa agc cct atg Val Asp Glu Glu His Asp Phe Ser Tyr Lys Ser His Gln Ser Pro Met 230 235 240			776
tat aac gct agg gat tta tgc ttg tat tta tct cat aaa ttc cct att Tyr Asn Ala Arg Asp Leu Cys Leu Tyr Leu Ser His Lys Phe Pro Ile 245 250 255			824
caa gtg atc tta ggc tct gct acg cca agt ttg aat agt tat aaa cgc Gln Val Ile Leu Gly Ser Ala Thr Pro Ser Leu Asn Ser Tyr Lys Arg 260 265 270			872
ttt aaa gat aag gct tta gtg cgc tta aag ggg cgc tac acc ccc acg Phe Lys Asp Lys Ala Leu Val Arg Leu Lys Gly Arg Tyr Thr Pro Thr 275 280 285 290			920
caa aaa aac att att ttt gaa aaa acc gag cgt ttt atc acg ccc aaa Gln Lys Asn Ile Ile Phe Glu Lys Thr Glu Arg Phe Ile Thr Pro Lys 295 300 305			968
ctc cta gaa gcg cta caa caa gtc cta gac aaa aac gag caa gcc att Leu Leu Glu Ala Leu Gln Gln Val Leu Asp Lys Asn Glu Gln Ala Ile 310 315 320			1016
att ttt gtg cct aca agg gct aat ttc aaa acc ttg ctg tgc caa agt Ile Phe Val Pro Thr Arg Ala Asn Phe Lys Thr Leu Leu Cys Gln Ser 325 330 335			1064
tgt tac aaa agc gtt caa tgc ccc ttt tgc agc gtg aat atg agc ttg			1112

00655913-062901 ET 555860

Cys	Tyr	Lys	Ser	Val	Gln	Cys	Pro	Phe	Cys	Ser	Val	Asn	Met	Ser	Leu		
340						345					350						
cat	tta	aag	acc	aac	aaa	ctc	atg	tgc	cat	tat	tgc	cat	ttt	tca	agc	1160	
His	Leu	Lys	Thr	Asn	Lys	Leu	Met	Cys	His	Tyr	Cys	His	Phe	Ser	Ser		
355					360					365					370		
cct	atc	cct	aaa	att	tgc	agc	gcg	tgt	caa	agc	gaa	gtc	tta	gtg	ggc	1208	
Pro	Ile	Pro	Lys	Ile	Cys	Ser	Ala	Cys	Gln	Ser	Glu	Val	Leu	Val	Gly		
				375					380					385			
aaa	agg	ata	ggc	act	atg	caa	gtg	cta	aag	gaa	tta	gag	agc	ctt	tta	1256	
Lys	Arg	Ile	Gly	Thr	Met	Gln	Val	Leu	Lys	Glu	Leu	Glu	Ser	Leu	Leu		
			390					395					400				
gag	ggg	gct	aaa	ata	gcg	att	tta	gat	aaa	gat	cac	act	agc	acg	caa	1304	
Glu	Gly	Ala	Lys	Ile	Ala	Ile	Leu	Asp	Lys	Asp	His	Thr	Ser	Thr	Gln		
		405					410					415					
aaa	aaa	ctc	cac	aat	att	tta	aac	gat	ttc	aac	gct	caa	aaa	acg	aat	1352	
Lys	Lys	Leu	His	Asn	Ile	Leu	Asn	Asp	Phe	Asn	Ala	Gln	Lys	Thr	Asn		
		420				425					430						
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Ile	Leu	Ile	Gly	Thr	Gln	Met	Ile	Ser	Lys	Gly	His	Asp	Tyr	Ala	Lys		
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Val	Ser	Leu	Ala	Val	Val	Leu	Gly	Ile	Asp	Asn	Ile	Ile	Lys	Ser	Asn		
				455					460					465			
agt	tat	agg	gct	tta	gaa	gaa	ggc	gtg	tcg	tta	ctt	tat	caa	atc	gct	1496	
Ser	Tyr	Arg	Ala	Leu	Glu	Glu	Gly	Val	Ser	Leu	Leu	Tyr	Gln	Ile	Ala		
			470					475					480				
ggg	agg	agc	gct	agg	caa	att	tct	ggc	caa	gtg	ttc	att	caa	agc	acc	1544	
Gly	Arg	Ser	Ala	Arg	Gln	Ile	Ser	Gly	Gln	Val	Phe	Ile	Gln	Ser	Thr		
			485				490					495					
gaa	acc	gat	ctg	tta	gaa	aat	ttc	tta	gaa	gat	tat	gaa	gat	ttt	tta	1592	
Glu	Thr	Asp	Leu	Leu	Glu	Asn	Phe	Leu	Glu	Asp	Tyr	Glu	Asp	Phe	Leu		
			500			505					510						
caa	tac	gaa	ttg	caa	gaa	agg	tgc	gaa	ctc	tac	ccg	cct	ttt	tct	agg	1640	
Gln	Tyr	Glu	Leu	Gln	Glu	Arg	Cys	Glu	Leu	Tyr	Pro	Pro	Phe	Ser	Arg		
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ctg	tgt	ttg	ttg	gag	ttt	aag	cat	aaa	aac	gaa	gaa	aaa	gcc	caa	caa	1688	
Leu	Cys	Leu	Leu	Glu	Phe	Lys	His	Lys	Asn	Glu	Glu	Lys	Ala	Gln	Gln		
				535					540					545			
ttg	agc	cta	aaa	gcc	tct	caa	acc	ctt	tct	tcg	tgt	tta	gaa	aag	ggc	1736	
Leu	Ser	Leu	Lys	Ala	Ser	Gln	Thr	Leu	Ser	Ser	Cys	Leu	Glu	Lys	Gly		
			550					555					560				
gta	acg	ctc	tct	aat	ttc	aaa	gcc	ccc	att	gaa	aaa	atc	gct	tct	tct	1784	
Val	Thr	Leu	Ser	Asn	Phe	Lys	Ala	Pro	Ile	Glu	Lys	Ile	Ala	Ser	Ser		
			565				570					575					

tat	cgc	tac	ctt	att	tta	ttg	cgt	tcc	aaa	aac	cct	tta	agc	cta	atc	1832
Tyr	Arg	Tyr	Leu	Ile	Leu	Leu	Arg	Ser	Lys	Asn	Pro	Leu	Ser	Leu	Ile	
	580					585					590					

aaa	agc	gtg	cat	gcg	ttt	tta	aaa	tcc	gcc	cct	agt	atc	cct	tgc	agc	1880
Lys	Ser	Val	His	Ala	Phe	Leu	Lys	Ser	Ala	Pro	Ser	Ile	Pro	Cys	Ser	
	595				600					605					610	

gtg	aac	atg	gat	cct	gtg	gat	att	ttt	taaaaaactc	atgttttata	1927
Val	Asn	Met	Asp	Pro	Val	Asp	Ile	Phe			
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Pro	Leu	Arg	Asn	Lys	Thr	Leu	Leu	Gly	Val	Val	Leu	Glu	Glu	Val	Ser
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Lys	Pro	Ser	Phe	Glu	Cys	Leu	Glu	Leu	Glu	Lys	Thr	Pro	Tyr	Phe	Leu
	50					55					60				
Leu	Pro	Phe	Gln	Met	Glu	Leu	Ala	Ile	Phe	Ile	Ala	Gln	Tyr	Tyr	Ser
65					70					75					80
Ala	Asn	Leu	Ser	Ser	Val	Leu	Ser	Leu	Phe	Ala	Pro	Phe	Lys	Glu	Cys
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Asp	Leu	Val	Gly	Leu	Glu	Lys	Ile	Glu	Pro	Ile	Leu	Asn	Ile	Leu	Ser
			100					105					110		
Gln	Thr	Gln	Thr	Asn	Ala	Leu	Lys	Glu	Leu	Gln	Lys	His	Ser	Ala	Ser
			115				120					125			
Leu	Leu	Phe	Gly	Asp	Thr	Gly	Ser	Gly	Lys	Thr	Glu	Ile	Tyr	Met	His
	130					135					140				
Ala	Ile	Ala	Gln	Thr	Leu	Glu	Gln	Lys	Lys	Ser	Ala	Leu	Leu	Leu	Val
145					150					155					160
Pro	Glu	Ile	Ala	Leu	Thr	Pro	Gln	Met	Gln	Gln	Arg	Leu	Lys	Arg	Val
				165					170					175	
Phe	Lys	Glu	Asn	Leu	Gly	Leu	Trp	His	Ser	Lys	Leu	Ser	Gln	Asn	Gln
			180					185					190		
Lys	Lys	Gln	Phe	Leu	Glu	Lys	Leu	Tyr	Ser	Gln	Glu	Ile	Lys	Leu	Val
		195					200					205			
Val	Gly	Thr	Arg	Ser	Ala	Leu	Phe	Leu	Pro	Leu	Lys	Glu	Leu	Gly	Leu
	210					215					220				
Ile	Ile	Val	Asp	Glu	Glu	His	Asp	Phe	Ser	Tyr	Lys	Ser	His	Gln	Ser
225					230					235					240
Pro	Met	Tyr	Asn	Ala	Arg	Asp	Leu	Cys	Leu	Tyr	Leu	Ser	His	Lys	Phe
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Pro	Ile	Gln	Val	Ile	Leu	Gly	Ser	Ala	Thr	Pro	Ser	Leu	Asn	Ser	Tyr
			260					265					270		
Lys	Arg	Phe	Lys	Asp	Lys	Ala	Leu	Val	Arg	Leu	Lys	Gly	Arg	Tyr	Thr
		275					280					285			
Pro	Thr	Gln	Lys	Asn	Ile	Ile	Phe	Glu	Lys	Thr	Glu	Arg	Phe	Ile	Thr
	290					295					300				
Pro	Lys	Leu	Leu	Glu	Ala	Leu	Gln	Gln	Val	Leu	Asp	Lys	Asn	Glu	Gln

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Gln	Ser	Cys	Tyr	Lys	Ser	Val	Gln	Cys	Pro	Phe	Cys	Ser	Val	Asn	Met	
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Ser	Leu	His	Leu	Lys	Thr	Asn	Lys	Leu	Met	Cys	His	Tyr	Cys	His	Phe	
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Ser	Ser	Pro	Ile	Pro	Lys	Ile	Cys	Ser	Ala	Cys	Gln	Ser	Glu	Val	Leu	
	370					375					380					
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Leu	Leu	Glu	Gly	Ala	Lys	Ile	Ala	Ile	Leu	Asp	Lys	Asp	His	Thr	Ser	
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Thr	Gln	Lys	Lys	Leu	His	Asn	Ile	Leu	Asn	Asp	Phe	Asn	Ala	Gln	Lys	
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Thr	Asn	Ile	Leu	Ile	Gly	Thr	Gln	Met	Ile	Ser	Lys	Gly	His	Asp	Tyr	
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Ala	Lys	Val	Ser	Leu	Ala	Val	Val	Leu	Gly	Ile	Asp	Asn	Ile	Ile	Lys	
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Ser	Asn	Ser	Tyr	Arg	Ala	Leu	Glu	Glu	Gly	Val	Ser	Leu	Leu	Tyr	Gln	
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Ile	Ala	Gly	Arg	Ser	Ala	Arg	Gln	Ile	Ser	Gly	Gln	Val	Phe	Ile	Gln	
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Ser	Thr	Glu	Thr	Asp	Leu	Leu	Glu	Asn	Phe	Leu	Glu	Asp	Tyr	Glu	Asp	
			500					505					510			
Phe	Leu	Gln	Tyr	Glu	Leu	Gln	Glu	Arg	Cys	Glu	Leu	Tyr	Pro	Pro	Phe	
		515					520					525				
Ser	Arg	Leu	Cys	Leu	Leu	Glu	Phe	Lys	His	Lys	Asn	Glu	Glu	Lys	Ala	
	530					535					540					
Gln	Gln	Leu	Ser	Leu	Lys	Ala	Ser	Gln	Thr	Leu	Ser	Ser	Cys	Leu	Glu	
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Ser	Ser	Tyr	Arg	Tyr	Leu	Ile	Leu	Leu	Arg	Ser	Lys	Asn	Pro	Leu	Ser	
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Leu	Ile	Lys	Ser	Val	His	Ala	Phe	Leu	Lys	Ser	Ala	Pro	Ser	Ile	Pro	
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Met Lys Leu Ser Ile Asn Asp Leu Asn Val	
1 5 10	
ttt gtc aat acg cct aaa gat ata gcc aaa ctc tgt gag gat ttg agt	159
Phe Val Asn Thr Pro Lys Asp Ile Ala Lys Leu Cys Glu Asp Leu Ser	
15 20 25	

aca Thr	acc Thr	cct Pro	atg Met 270	gat Asp	ttg Leu	agc Ser	gtg Val	aaa Lys 275	aac Asn	gat Asp	gaa Glu	aac Asn	aac Asn	ctt Leu	gaa Glu	927
agc Ser	gtt Val	tat Tyr 285	atc Ile	aac Asn	cat His	caa Gln	aaa Lys 290	cgc Arg	tcc Ser	acg Thr	atc Ile	gct Ala 295	atc Ile	aag Lys	cat His	975
caa Gln	gtt Val 300	caa Gln	aaa Lys	gat Asp	ttg Leu	agc Ser 305	gag Glu	tgt Cys	ttg Leu	ctt Leu	tta Leu 310	gag Glu	gca Ala	agt Ser	tac Tyr	1023
acc Thr 315	gat Asp	ccg Pro	ata Ile	agc Ser	ctg Leu 320	tct Ser	tta Leu	aaa Lys	tta Leu	cac His 325	gcc Ala	cta Leu	aaa Lys	gat Asp	aaa Lys 330	1071
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gta Val 395	gag Glu	aaa Lys	gaa Glu	aaa Lys	att Ile 400	caa Gln	ggc Gly	att Ile	tta Leu	aaa Lys 405	aat Asn	tta Leu	ggc Gly	ttt Phe	aaa Lys 410	1311
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gaa Glu	att Ile	ttg Leu 445	cgc Arg	ttt Phe	gta Val	ggg Gly	att Ile 450	gat Asp	aat Asn	cta Leu	gtc Val	tca Ser 455	aag Lys	ccc Pro	ctt Leu	1455
cat His	tgt Cys 460	gtc Val	agt Ser	agc Ser	aaa Lys	aat Asn 465	tca Ser	aac Asn	ccc Pro	aat Asn	tac Tyr 470	gac Asp	acg Thr	cac His	cgc Arg	1503
ttt Phe 475	ttt Phe	gaa Glu	aac Asn	ctt Leu	aaa Lys 480	cac His	aag Lys	gct Ala	ctc Leu	gct Ala 485	tgc Cys	ggg Gly	ttt Phe	aaa Lys	gaa Glu 490	1551
gtc Val	att Ile	catt His	tac Tyr	gtg Val	ttt Phe	tac Tyr	tct Ser	aaa Lys	gaa Glu	aaa Lys	cag Gln	caa Gln	aaa Lys	tta Leu	ggc Gly	1599

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Ser	Leu	Arg	Asn	Lys	Asn	Leu	Gly	Phe	Lys	Ser	Ile	Ala	Leu	Tyr	Glu	
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Gly	Lys	Ala	Trp	Asp	Phe	Tyr	Ser	Phe	Ala	Glu	Cys	Val	Ser	Lys	Val	
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Ile	Gly	Asp	Phe	Ser	Leu	Glu	Lys	Leu	Thr	Thr	Gln	Thr	Pro	Ile	Asn	
			605				610						615			
cac	ccc	tac	cag	agc	gct	aaa	atc	att	caa	aat	cat	gaa	atc	ata	ggc	1983
His	Pro	Tyr	Gln	Ser	Ala	Lys	Ile	Ile	Gln	Asn	His	Glu	Ile	Ile	Gly	
			620				625						630			
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Val	Ile	Ala	Lys	Ile	His	Pro	Lys	Val	Ile	Gln	Glu	Leu	Asp	Leu	Phe	
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Glu	Ser	Tyr	Tyr	Ala	Glu	Ile	Asp	Ala	Phe	Lys	Leu	Lys	Arg	Pro	Ala	
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Met	Leu	Leu	Lys	Pro	Phe	Ser	Ile	Tyr	Pro	Ser	Ser	Val	Arg	Asp	Leu	
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Thr	Leu	Ile	Ile	Asp	Glu	Asn	Thr	Ala	Phe	Ser	Gly	Ile	Lys	Lys	Ala	
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Leu	Lys	Asp	Ala	Gln	Ile	Pro	Asn	Leu	Ser	Glu	Ile	Leu	Pro	Leu	Asp	
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Ile	Phe	Lys	Glu	Ser	Asn	Asn	Ser	Ile	Ala	Leu	Ser	Val				

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735 740 745

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Val Gln Lys Ala Leu Glu Ile Leu Glu Lys Glu Phe Asn Ala Arg Leu
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35 40 45
Ile Leu Glu Lys Ala Pro His Lys Asn Ala Glu Lys Leu Ser Val Cys
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Gln Val Asp Val Gly Lys Glu Val Leu Gln Ile Val Cys Gly Ala Lys
65 70 75 80
Asn Val Ala Pro Asn Gln Phe Val Pro Val Ala Leu Asn Gly Ala Leu
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Ile Gly Ser Thr Thr Ile Ala Lys Thr Glu Leu Arg Gly Val Glu Ser
100 105 110
His Gly Met Ile Cys Ser Ser Ile Glu Leu Gly Phe Pro Lys Ile Asn
115 120 125
Asp Gly Ile Leu Glu Leu Asp Glu Ser Val Gly Glu Leu Val Leu Gly
130 135 140
Lys Glu Leu Asn Glu Tyr Ala Pro Phe Asn Thr His Val Leu Glu Ile
145 150 155 160
Ser Leu Thr Pro Asn Arg Gly Asp Cys Leu Ser Val Leu Gly Ile Ala
165 170 175
Arg Glu Ile Ser Ala Phe Tyr His Thr Pro Leu Lys Pro Ile Lys Ala
180 185 190
Leu Asn Phe Thr Pro Lys Ser Gly Leu Ile Thr Leu Ser Ala Gly Glu
195 200 205
Asn Ile Glu Ser His Leu Ala Tyr Tyr Leu Ile Cys Asn His Ser Leu
210 215 220
Lys Thr Pro Leu Asn Ile Lys Leu Ser Leu Ala His Asn Asn Ala Leu
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Ser Glu Asn Asp Leu Asn Asn Phe Ile Glu Phe Ser Thr His Phe Ser
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Gly Val Ile Met Asn Ala Tyr Ser Leu Asn Thr Thr Pro Met Asp Leu
260 265 270
Ser Val Lys Asn Asp Glu Asn Asn Leu Glu Ser Val Tyr Ile Asn His
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Gln Lys Arg Ser Thr Ile Ala Ile Lys His Gln Val Gln Lys Asp Leu
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Glu	Asp	Ile	Thr	Glu	Ile	Leu	Gly	Leu	Ala	Val	Glu	Lys	Glu	Lys	Ile	
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Gln	Gly	Ile	Leu	Lys	Asn	Leu	Gly	Phe	Lys	Val	Ser	Val	Lys	Glu	Pro	
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Asn	Ser	Asn	Pro	Asn	Tyr	Asp	Thr	His	Arg	Phe	Phe	Glu	Asn	Leu	Lys	
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Tyr	Ser	Lys	Glu	Lys	Gln	Gln	Lys	Leu	Gly	Phe	Glu	Val	Leu	Glu	Asp	
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Gln	Lys	Lys	Glu	Ser	Tyr	Pro	Asp	Thr	Lys	Gly	Lys	Ala	Trp	Asp	Phe	
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		675					680					685				
Asn	Thr	Ala	Phe	Ser	Gly	Ile	Lys	Lys	Ala	Leu	Lys	Asp	Ala	Gln	Ile	
	690					695					700					
Pro	Asn	Leu	Ser	Glu	Ile	Leu	Pro	Leu	Asp	Ile	Phe	Lys	Glu	Ser	Asn	
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Thr	Leu	Asn	Asp	Glu	Glu	Val	Asn	Ser	Ala	Val	Gln	Lys	Ala	Leu	Glu	
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[illegible]

-383-

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 <213> Helicobacter pylori

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 35 40 45
 His Thr Pro Met Phe His Gln Ile Glu Gly Leu Val Val Asp Gln Lys
 50 55 60
 Gly Asn Ile Arg Phe Thr His Leu Lys Gly Val Ile Glu Asp Phe Leu
 65 70 75 80
 His Tyr Phe Phe Gly Gly Val Lys Leu Arg Trp Arg Ser Ser Phe Phe
 85 90 95
 Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Ile Ser Cys Val Phe Cys
 100 105 110
 Lys Gln Glu Gly Cys Arg Val Cys Ser His Thr Gly Trp Leu Glu Val
 115 120 125
 Leu Gly Cys Gly Met Val Asn Ala Val Phe Glu Ala Ile Gly Tyr
 130 135 140
 Glu Asn Val Ser Gly Phe Ala Phe Gly Met Gly Ile Glu Arg Leu Ala
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 Met Leu Thr Cys Gln Ile Asn Asp Leu Arg Ser Phe Phe Glu Thr Asp
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 Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu Met His
 5 10 15

gtg cat ttt gta ttt gtt act aaa tac agg cgt tca gca ttc aat aag 152
 Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe Asn Lys
 20 25 30

0055913-062901 ET 656360

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 Glu Val Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys Lys Asp
 35 40 45 50

ttt gag agc gaa ttg gta gaa ttt gat ggg gag agc gat cat gtg cat 248
 Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His Val His
 55 60 65

ttg ctt atc aac tac cct cca aaa gtg agc gtg agt aag tta gtt aat 296
 Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu Val Asn
 70 75 80

tct tta aaa ggc gtt agc agt cgt ttg act aga caa cac cat ttc aaa 344
 Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His Phe Lys
 85 90 95

agc gtt gaa gct agt ttg tgg ggg aag cat tta tgg tcg cct agt tat 392
 Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro Ser Tyr
 100 105 110

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 Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys Gln Tyr
 115 120 125 130

ata caa gat caa gaa aca ccg cat taaattagct aactttgatt tttaagtaga 494
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 35 40 45
 Lys Asp Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His
 50 55 60
 Val His Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu
 65 70 75 80
 Val Asn Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His
 85 90 95
 Phe Lys Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro
 100 105 110
 Ser Tyr Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys
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 Gln Tyr Ile Gln Asp Gln Glu Thr Pro His
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 <212> DNA

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<400> 333

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agc Ser	agc Ser	act Thr	gaa Glu	gtt Val 215	tta Leu	gag Glu	gcg Ala	atg Met	cgc Arg 220	ctt Leu	tta Leu	gaa Glu	gaa Glu	aac Asn 225	gac Asp	728
ttg Leu	tta Leu	gag Glu	cat His 230	ttc Phe	cac His	atg Met	ata Ile	cat His 235	ttc Phe	cat His	ata Ile	ggc Gly	tct Ser 240	caa Gln	atc Ile	776
agc Ser	gat Asp	att Ile 245	tcg Ser	ccc Pro	tta Leu	aaa Lys	aag Lys 250	gct Ala	tta Leu	aga Arg	gaa Glu	gcg Ala 255	ggt Gly	aac Asn	ttg Leu	824
tat Tyr	gca Ala 260	gaa Glu	ttg Leu	cgt Arg	aaa Lys	atg Met 265	ggc Gly	gct Ala	aaa Lys	aat Asn	ctt Leu 270	aat Asn	agc Ser	gtg Val	aat Asn	872
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gac Asp	aaa Lys	aac Asn	tac Tyr	act Thr 295	tta Leu	gag Glu	gaa Glu	ttc Phe	agc Ser 300	gct Ala	gat Asp	gtg Val	gtg Val	ttt Phe 305	tta Leu	968
ttg Leu	aga Arg	gaa Glu	att Ile 310	gtg Val	aaa Lys	aat Asn	aag Lys	cag Gln 315	gaa Glu	atc Ile	gag Glu	ccg Pro	gac Asp 320	att Ile	ttc Phe	1016
att Ile	gaa Glu	tca Ser 325	ggc Gly	cgt Arg	tat Tyr	att Ile	tcc Ser 330	gct Ala	aac Asn	cat His	gcc Ala	gtt Val 335	tta Leu	gtg Val	gcc Ala	1064
ccg Pro	gtg Val 340	tta Leu	gaa Glu	ttg Leu	ttt Phe	tcg Ser 345	cat His	gaa Glu	tac Tyr	aat Asn	gaa Glu 350	aaa Lys	tcc Ser	cta Leu	aaa Lys	1112
atc Ile 355	aaa Lys	gaa Glu	aat Asn	aat Asn	aac Asn 360	ccc Pro	cct Pro	ttg Leu	att Ile	gat Asp 365	gaa Glu	atg Met	cta Leu	gac Asp	ttg Leu 370	1160
ctc Leu	gct Ala	aat Asn	atc Ile	aat Asn 375	gaa Glu	aaa Lys	aac Asn	gcc Ala	att Ile 380	gaa Glu	tac Tyr	ttg Leu	cat His	gat Asp 385	agt Ser	1208
ttt Phe	gat Asp	cac His	acc Thr 390	gag Glu	tcg Ser	cta Leu	ttc Phe	acg Thr 395	ctt Leu	ttt Phe	gat Asp	ctg Leu	ggc Gly 400	tat Tyr	att Ile	1256
gat Asp	ttg Leu	att Ile 405	gac Asp	agg Arg	agc Ser	aac Asn	act Thr 410	gaa Glu	gtt Val	tta Leu	gcc Ala 415	cat His	ttg Leu	atc Ile	gtc Val	1304
aaa Lys	aaa Lys 420	gcg Ala	gtg Val	caa Gln	ttg Leu	ctt Leu 425	tat Tyr	gtt Val	aag Lys	gat Asp	cat His 430	aac Asn	gat Asp	att Ile	tta Leu	1352

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Arg Ile Gln Glu Gln Val Gln Glu Arg Tyr Leu Leu Asn Cys Ser Phe
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Phe Gln Ser Leu Pro Asp Tyr Trp Gly Leu Arg Gln Asn Phe Pro Val
455 460 465

atg ccc ttg aat aaa tta gat gaa aag ccc acc agg agt gcg agc ttg 1496
Met Pro Leu Asn Lys Leu Asp Glu Lys Pro Thr Arg Ser Ala Ser Leu
470 475 480

tgg gat att act tgc gat agc gat ggg gaa atc gct ttt gat tcc acg 1544
Trp Asp Ile Thr Cys Asp Ser Asp Gly Glu Ile Ala Phe Asp Ser Thr
485 490 495

aag ccc ttg ttt ttg cac gat ata gat ata gat gaa gaa gaa tac ttt 1592
Lys Pro Leu Phe Leu His Asp Ile Asp Ile Asp Glu Glu Glu Tyr Phe
500 505 510

tta gcg ttc ttt tta gtg gga gcg tat caa gaa gtt tta ggc atg aaa 1640
Leu Ala Phe Phe Leu Val Gly Ala Tyr Gln Glu Val Leu Gly Met Lys
515 520 525 530

cac aat tta ttc acg cac cta cgg aat tta gcg tgg ttt ttg atg aaa 1688
His Asn Leu Phe Thr His Leu Arg Asn Leu Ala Trp Phe Leu Met Lys
535 540 545

aag gcg att atg aag tgg aag ata ttt gtg aag ccc aaa cga ttt 1733
Lys Ala Ile Met Lys Trp Lys Ile Phe Val Lys Pro Lys Arg Phe
550 555 560

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<213> Helicobacter pylori

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35 40 45
Pro Leu Leu Val Arg Phe Pro His Leu Val Gln Lys Gln Ile Lys Ser
50 55 60
Leu Phe Asp Ala Phe Ser Ser Ala Ile Lys Glu Tyr Gln Tyr Ser Gly
65 70 75 80
Ala Phe Lys Ala Val Phe Pro Leu Lys Val Asn Gln Met Pro Ser Phe
85 90 95
Val Phe Pro Leu Val Gln Gly Ala Lys Gly Leu Asn Tyr Gly Leu Glu
100 105 110
Ala Gly Ser Lys Ser Glu Leu Ile Ala Met Ser Tyr Thr Asn Pro
115 120 125
Lys Ala Pro Ile Thr Val Asn Gly Phe Lys Asp Lys Glu Met Ile Glu
130 135 140

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Glu	Gly	Leu	Asn	Glu	Leu	Lys	Thr	Ile	Ile	Ala	Val	Ala	Lys	Gln	Asn
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Glu	Phe	Leu	Ala	Cys	Pro	Lys	Ile	Gly	Ile	Arg	Ile	Arg	Leu	His	Ser
			180						185						190
Thr	Gly	Thr	Gly	Val	Trp	Ala	Lys	Ser	Gly	Gly	Ile	Asn	Ser	Lys	Phe
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Gly	Leu	Ser	Ser	Thr	Glu	Val	Leu	Glu	Ala	Met	Arg	Leu	Leu	Glu	Glu
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Asn	Asp	Leu	Leu	Glu	His	Phe	His	Met	Ile	His	Phe	His	Ile	Gly	Ser
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Gln	Ile	Ser	Asp	Ile	Ser	Pro	Leu	Lys	Lys	Ala	Leu	Arg	Glu	Ala	Gly
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Val	Asn	Ile	Gly	Gly	Gly	Leu	Ala	Val	Glu	Tyr	Thr	Gln	His	Lys	His
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His	Gln	Asp	Lys	Asn	Tyr	Thr	Leu	Glu	Glu	Phe	Ser	Ala	Asp	Val	Val
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Val	Ala	Pro	Val	Leu	Glu	Leu	Phe	Ser	His	Glu	Tyr	Asn	Glu	Lys	Ser
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Leu	Lys	Ile	Lys	Glu	Asn	Asn	Asn	Pro	Pro	Leu	Ile	Asp	Glu	Met	Leu
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Asp	Leu	Leu	Ala	Asn	Ile	Asn	Glu	Lys	Asn	Ala	Ile	Glu	Tyr	Leu	His
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Asp	Ser	Phe	Asp	His	Thr	Glu	Ser	Leu	Phe	Thr	Leu	Phe	Asp	Leu	Gly
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Tyr	Ile	Asp	Leu	Ile	Asp	Arg	Ser	Asn	Thr	Glu	Val	Leu	Ala	His	Leu
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Ile	Val	Lys	Lys	Ala	Val	Gln	Leu	Leu	Tyr	Val	Lys	Asp	His	Asn	Asp
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Ile	Leu	Arg	Ile	Gln	Glu	Gln	Val	Gln	Glu	Arg	Tyr	Leu	Leu	Asn	Cys
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Ser	Phe	Phe	Gln	Ser	Leu	Pro	Asp	Tyr	Trp	Gly	Leu	Arg	Gln	Asn	Phe
	450					455					460				
Pro	Val	Met	Pro	Leu	Asn	Lys	Leu	Asp	Glu	Lys	Pro	Thr	Arg	Ser	Ala
465					470					475					480
Ser	Leu	Trp	Asp	Ile	Thr	Cys	Asp	Ser	Asp	Gly	Glu	Ile	Ala	Phe	Asp
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Ser	Thr	Lys	Pro	Leu	Phe	Leu	His	Asp	Ile	Asp	Ile	Asp	Glu	Glu	Glu
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Tyr	Phe	Leu	Ala	Phe	Phe	Leu	Val	Gly	Ala	Tyr	Gln	Glu	Val	Leu	Gly
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Met	Lys	His	Asn	Leu	Phe	Thr	His	Leu	Arg	Asn	Leu	Ala	Trp	Phe	Leu
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Phe															

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Thr	Glu	Asn	Gln	Lys	Lys	Ala	Ile	Lys	Ile	Ala	Leu	Asn	Thr	Pro	Asp
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Asn	Ala	Ile	Cys	Glu	Arg	Leu	Phe	Glu	Glu	Tyr	Pro	Lys	Asp	Lys	Asn
65					70					75					80
Ile	Lys	Gly	Gln	Ile	Leu	Leu	Cys	Ala	Gln	Gly	His	Asp	Ala	Thr	Asn
				85					90					95	
Asn	Ala	Arg	Glu	Arg	Ile	Lys	Val	Gly	Gly	Leu	Pro	Thr	Phe	Lys	Phe
			100					105					110		
Gly	Ala	Lys	Lys	Asn	Ala	Lys	Glu	Glu	Gln	Tyr	Lys	Gln	Asp	Glu	Arg
		115					120					125			
Leu	Asn	Glu	Arg	Leu	Arg	Glu	Phe	Ala	Glu	Thr	Leu	Ile	Glu	Ser	Val
	130					135					140				
Arg	Lys	Lys	Leu	Gln	Lys	Leu	Gly	Asp	Tyr	Glu	Asn	Ile	Glu	Lys	Ile
145					150					155					160
Leu	Asp	Leu	Glu	Glu	Ala	Leu	Arg	Arg	Tyr	Tyr	Ser	Ser	Pro	Ile	Ser
				165					170					175	
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Val Leu Asp Ala Asn Ile Leu Lys Glu Met His Ala Asn Asn Val Cys						
10 15 20 25						
tat tcc aag cat tca aaa gat agg ttt att cct ttc aaa ttt gat aaa	208					
Tyr Ser Lys His Ser Lys Asp Arg Phe Ile Pro Phe Lys Phe Asp Lys						
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ttt ggt tat gtt gga tgt aaa ctt ttt aaa aag ata tta aac ttt cct	256					
Phe Gly Tyr Val Gly Cys Lys Leu Phe Lys Lys Ile Leu Asn Phe Pro						
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Ser	Asn	Thr	Thr	Phe	Phe	Gly	Gly	Thr	Gly	Cys	Lys	Lys	Leu	Met	Glu		
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Leu	Leu	Ser	Glu	Ile	Val	Ile	Asp	Ser	Arg	Ser	Ser	Lys	Ile	Ala	Leu		
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Asn	Arg	His	Tyr	Ala	Leu	Thr	Arg	Leu	Gln	Trp	Cys	Asp	Arg	Thr	Leu		
	90				95					100					105		
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Arg	His	Asn	Leu	Gln	Ile	Leu	Glu	Arg	Ile	Gly	Phe	Leu	Thr	Ala	Phe		
				110					115					120			
aag	aac	aaa	aaa	ggg	tat	att	ttt	ttg	tct	atg	cat	gac	ttc	act	aaa		496
Lys	Asn	Lys	Lys	Gly	Tyr	Ile	Phe	Leu	Ser	Met	His	Asp	Phe	Thr	Lys		
			125					130					135				
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Ile	Glu	Asn	Tyr	Glu	His	Ser	Gly	Leu	Asn	Gly	Glu	Ser	Asn	Leu	Pro		
		140					145					150					
aat	agc	ttc	ttt	tta	gga	att	tgt	ggg	tat	ttg	aaa	aaa	ctc	ttc	aag		592
Asn	Ser	Phe	Phe	Leu	Gly	Ile	Cys	Gly	Tyr	Leu	Lys	Lys	Leu	Phe	Lys		
	155					160					165						
aaa	tta	aaa	gat	aga	gca	ttc	agg	ctc	gca	aac	aag	cac	ggg	gta	ttc		640
Lys	Leu	Lys	Asp	Arg	Ala	Phe	Arg	Leu	Ala	Asn	Lys	His	Gly	Val	Phe		
	170				175					180				185			
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Phe	Leu	Lys	Ile	Pro	Lys	His	Phe	Gln	Met	Gln	Asn	Phe	Asn	Asn	Ile		
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Phe	Leu	Glu	Phe	Val	Ser	Val	Asn	Asn	Pro	Cys	Phe	Ser	Tyr	Arg	Leu		
			205					210						215			
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Thr	Tyr	Asp	Gln	Leu	Val	Gly	Lys	Lys	Ile	Pro	Asn	Ile	Lys	Cys	Ser		
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Tyr	Gln	Gln	Ala	Ile	Val	Lys	Lys	Asn	Ile	His	Arg	Ala	Leu	Asp	Glu		
	235					240					245						
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Leu	Ser	Ile	Asp	Lys	Glu	Ile	Leu	Ala	Ser								
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 Leu Phe Lys Lys Ile Leu Asn Phe Pro Ser Asn Thr Thr Phe Phe Gly
 50 55 60
 Gly Thr Gly Cys Lys Lys Leu Met Glu Leu Leu Ser Glu Ile Val Ile
 65 70 75 80
 Asp Ser Arg Ser Ser Lys Ile Ala Leu Asn Arg His Tyr Ala Leu Thr
 85 90 95
 Arg Leu Gln Trp Cys Asp Arg Thr Leu Arg His Asn Leu Gln Ile Leu
 100 105 110
 Glu Arg Ile Gly Phe Leu Thr Ala Phe Lys Asn Lys Lys Gly Tyr Ile
 115 120 125
 Phe Leu Ser Met His Asp Phe Thr Lys Ile Glu Asn Tyr Glu His Ser
 130 135 140
 Gly Leu Asn Gly Glu Ser Asn Leu Pro Asn Ser Phe Phe Leu Gly Ile
 145 150 155 160
 Cys Gly Tyr Leu Lys Lys Leu Phe Lys Lys Leu Lys Asp Arg Ala Phe
 165 170 175
 Arg Leu Ala Asn Lys His Gly Val Phe Phe Leu Lys Ile Pro Lys His
 180 185 190
 Phe Gln Met Gln Asn Phe Asn Asn Ile Phe Leu Glu Phe Val Ser Val
 195 200 205
 Asn Asn Pro Cys Phe Ser Tyr Arg Leu Thr Tyr Asp Gln Leu Val Gly
 210 215 220
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 <213> Helicobacter pylori
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 Ser Phe Leu Arg Ser Ile Ala Phe Phe Asp Asp Phe Ser Ala Ser Phe
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 Glu Tyr Arg Asp Leu Phe Ser Val Leu Glu Asn Ile Val Gln Phe Asp

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Tyr Glu Lys Lys Pro Tyr Lys Asp Asp Leu Tyr Phe Leu Cys Lys Phe	55	60	65	
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Val Glu Pro Ala Leu Lys Ala Ile Phe Ser Asn Leu Asn Thr Asn Ile	70	75	80	
tac cga aaa cat tta aaa atg cct tta gaa aag gct agg gaa ttt gac				344
Tyr Arg Lys His Leu Lys Met Pro Leu Glu Lys Ala Arg Glu Phe Asp	85	90	95	
gct aaa tgc gcg ttg gat tta gcc aag cga cca ggt cgt agt ttg aaa				392
Ala Lys Cys Ala Leu Asp Leu Ala Lys Arg Pro Gly Arg Ser Leu Lys	100	105	110	
gaa aag ttg tgc gac aat aaa gta ttg agc gtc aag cgt tat gtg aat				440
Glu Lys Leu Cys Asp Asn Lys Val Leu Ser Val Lys Arg Tyr Val Asn	115	120	125	130
gcc aat acg cat gaa aac agg ttt ctc aag cgt ttc att aaa gaa ctt				488
Ala Asn Thr His Glu Asn Arg Phe Leu Lys Arg Phe Ile Lys Glu Leu	135	140	145	
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Leu Arg Ile Ile His Trp Arg Glu Ile Glu Phe Gln Gln Val Phe Glu	150	155	160	
gag tta att ttc agc ata aca agt ttt tta aag aat gga gta gcc caa				584
Glu Leu Ile Phe Ser Ile Thr Ser Phe Leu Lys Asn Gly Val Ala Gln	165	170	175	
caa att gat gaa aaa caa gcc atc att cct aat aac ttg ttg cat ttt				632
Gln Ile Asp Glu Lys Gln Ala Ile Ile Pro Asn Asn Leu Leu His Phe	180	185	190	
gat aag cac tac aaa cgc att ttt aaa gcc cat gat tgg ctt tat gat				680
Asp Lys His Tyr Lys Arg Ile Phe Lys Ala His Asp Trp Leu Tyr Asp	195	200	205	210
ggt gtg ggg tca ttg atg aat ttg gat caa att ttc tat ttg gag tgt				728
Gly Val Gly Ser Leu Met Asn Leu Asp Gln Ile Phe Tyr Leu Glu Cys	215	220	225	
tta tac caa gcc caa ttt tat act tct aaa aac att gaa ccc acg cta				776
Leu Tyr Gln Ala Gln Phe Tyr Thr Ser Lys Asn Ile Glu Pro Thr Leu	230	235	240	
att aga aat gaa caa gat tta tac gcg cta att aaa aat agt ttt cca				824
Ile Arg Asn Glu Gln Asp Leu Tyr Ala Leu Ile Lys Asn Ser Phe Pro	245	250	255	
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Ile Lys Asp Leu Ser Phe Glu Lys Met Arg Leu Lys Ala Lys Glu Phe	260	265	270	
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Gln	Leu	Glu	Leu	Cys	Lys	Gly	Val	Tyr	Lys	Glu	Met	Tyr	Ile	Asp	Met	
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Lys	Ile	Leu	Lys	Leu	Pro	Leu	Leu	Val	Lys	Lys	Gln	Glu	Asn	Asn	Thr	
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Tyr	Ile	Asn	Ala	Asn	Gly	Ala	Lys	Gly	Lys	Ile	Asp	Glu	Lys	Gly	Tyr	
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Met	Arg	Asp	Phe	Lys	Glu	Arg	Tyr	Lys	Ile	Glu	Lys	Leu	Tyr	Tyr	Leu	
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Ile	Ser	Leu	Tyr	Phe	Lys	Asp	Ala	Lys	Phe	Tyr	Pro	Lys	Ser	Val	Ala	
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cga Arg	gaa Glu	agt Ser	ttt Phe 550	gct Ala	ttg Leu	ccc Pro	ttg Leu	atc Ile 555	cta Leu	aat Asn	gaa Glu	gaa Glu	aaa Lys 560	atc Ile	gcc Ala	1736
tat Tyr	caa Gln	ggt Gly 565	aaa Lys	atc Ile	acc Thr	tct Ser	aaa Lys 570	gat Asp	ttt Phe	ccc Pro	cta Leu	gaa Glu 575	aat Asn	gac Asp	gaa Glu	1784
gaa Glu	tac Tyr 580	aaa Lys	ctc Leu	acg Thr	ctc Leu	act Thr 585	tat Tyr	gac Asp	att Ile	ggc Gly 590	acc Thr	gag Glu	ttt Phe	aac Asn	tat Tyr	1832
gtg Val 595	tta Leu	gag Glu	ttt Phe	aaa Lys	cct Pro 600	gtc Val	aat Asn	aat Asn	gat Asp	tta Leu 605	aag Lys	ccc Pro	att Ile	gtc Val	atg Met 610	1880
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ggc Gly	aaa Lys 645	agt Ser	tct Ser	gat Asp	ttg Leu	ttt Phe	gag Glu 650	tgg Trp	gcg Ala	cta Leu	gag Glu	caa Gln 655	tta Leu	gag Glu	aca Thr	2024
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Ile	Lys	His	Arg	Ile	Glu	Ala	Leu	Lys	Arg	Ile	Lys	Tyr	Pro	Cys	Leu			
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Ser	Lys	Ile 35	Lys	Ser	Leu	Arg	Lys 40	Phe	Glu	Ser	Asn	Pro 45	Leu	Val	Arg
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Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser Pro Lys	
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acc agc act tct tgt ttg atg gat ttg agc ttg tca aaa tta aac tca	584
Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu Asn Ser	
165 170 175	
atg cct atc ata aac att aaa aag acg ata cca aat tcg cca ata tca	632
Met Pro Ile Ile Asn Ile Lys Lys Thr Ile Pro Asn Ser Pro Ile Ser	
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gac aac aaa tca aaa tca tta att tta aaa aaa gcc gct aag acc gtt	680
Asp Asn Lys Ser Lys Ser Leu Ile Leu Lys Lys Ala Ala Lys Thr Val	
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Tyr Pro Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser	
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Pro Lys Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu	
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Ala Gln Arg Val Ala Leu Ala Arg Ala Leu Ile Ala Ala Lys Asn Leu
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Val Leu Leu Val Ser His Asn Pro Asn Glu Ile Thr Lys Leu Ala Gln
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cgg ctt ttt tca aac cgc tta tta ata aaa cct ctc ttt gaa gat gaa 392
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Asn Tyr Cys His Tyr Glu Val Ile Ser Gln Thr Ile Ser Leu Pro Lys
115 120 125 130
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Gly	Gly	Leu	Arg	Thr	Ala	Ile	Phe	Asn	Tyr	Leu	Phe	Ala	Arg	Ala	Asn		
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Leu	Glu	Tyr	Asp	Gly	Glu	Ile	Leu	Tyr	Gln	Ser	Lys	Arg	Phe	Glu	Ile		
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Gly	Thr	Pro	Pro	Lys	Gly	Ile	Glu	Pro	Val	Val	Arg	Ile	Lys	Val	Pro		
				135					140					145			
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Gln	Asn	Glu	Val	Ile	Gly	Phe	Asn	Asp	Gly	Val	Lys	Gly	Glu	Val	Lys		
			150					155					160				
gtg	aat	act	aac	gaa	tta	gac	gat	ttt	att	atc	gcc	agg	agc	gat	ggg		585
Val	Asn	Thr	Asn	Glu	Leu	Asp	Asp	Phe	Ile	Ile	Ala	Arg	Ser	Asp	Gly		
		165					170					175					
aca	ccc	act	tat	aac	ttt	gtg	gtt	act	att	gat	gac	gct	tta	atg	ggg		633
Thr	Pro	Thr	Tyr	Asn	Phe	Val	Val	Thr	Ile	Asp	Asp	Ala	Leu	Met	Gly		
		180				185					190						
att	act	gat	gtg	att	aga	ggc	gat	gat	cac	ctt	tct	aac	acc	cct	aaa		681
Ile	Thr	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Leu	Ser	Asn	Thr	Pro	Lys		
195					200					205					210		
caa	atc	gtt	ctt	tat	aag	gct	ttg	aat	ttt	aaa	atc	cct	aat	ttt	ttc		729
Gln	Ile	Val	Leu	Tyr	Lys	Ala	Leu	Asn	Phe	Lys	Ile	Pro	Asn	Phe	Phe		
				215					220					225			
cat	gtg	ccg	atg	att	ttg	aat	gaa	gaa	ggg	caa	aaa	tta	agc	aaa	cgc		777
His	Val	Pro	Met	Ile	Leu	Asn	Glu	Glu	Gly	Gln	Lys	Leu	Ser	Lys	Arg		
			230				235					240					
cat	ggg	gcc	act	aat	gtg	atg	gac	tat	caa	gaa	atg	ggc	tat	ctt	aag		825
His	Gly	Ala	Thr	Asn	Val	Met	Asp	Tyr	Gln	Glu	Met	Gly	Tyr	Leu	Lys		
		245					250					255					
gaa	gct	tta	gtg	aat	ttt	tta	gcg	cgt	ttg	ggg	tgg	agc	tat	cag	gat		873
Glu	Ala	Leu	Val	Asn	Phe	Leu	Ala	Arg	Leu	Gly	Trp	Ser	Tyr	Gln	Asp		
		260				265					270						
aaa	gag	gtt	ttt	agc	atg	caa	gaa	ttg	cta	gaa	tta	ttt	gat	cct	aaa		921
Lys	Glu	Val	Phe	Ser	Met	Gln	Glu	Leu	Leu	Glu	Leu	Phe	Asp	Pro	Lys		
275					280					285					290		
gat	ttg	aat	tct	tcg	ccc	agt	tgc	ttc	agc	tgg	cac	aag	ctt	aat	tgg		969
Asp	Leu	Asn	Ser	Ser	Pro	Ser	Cys	Phe	Ser	Trp	His	Lys	Leu	Asn	Trp		
				295					300					305			
ctc	aac	gct	cat	tat	tta	aaa	aac	caa	agt	gtg	caa	gaa	ttg	tta	aaa		1017
Leu	Asn	Ala	His	Tyr	Leu	Lys	Asn	Gln	Ser	Val	Gln	Glu	Leu	Leu	Lys		
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Leu Leu Lys Pro Phe Ser Phe Ser Asp Leu Ser His Leu Asn Pro Thr
325 330 335

caa ttg gat cgc ttg tta gac gct ctc aaa gaa aga tct caa aca cta 1113
Gln Leu Asp Arg Leu Leu Asp Ala Leu Lys Glu Arg Ser Gln Thr Leu
340 345 350

aaa gaa tta gcc ctt aaa ata gat gag gtt tta atc gcc cct gtg gag 1161
Lys Glu Leu Ala Leu Lys Ile Asp Glu Val Leu Ile Ala Pro Val Glu
355 360 365 370

tat gaa gaa aag gtt ttt aaa aaa ctc aat caa gcg ctc gtt atg ccc 1209
Tyr Glu Glu Lys Val Phe Lys Lys Leu Asn Gln Ala Leu Val Met Pro
375 380 385

ttg tta gaa aag ttt aag cta gaa tta aac aaa gcc aat ttc aac gat 1257
Leu Leu Glu Lys Phe Lys Leu Glu Leu Asn Lys Ala Asn Phe Asn Asp
390 395 400

gaa agc gcg cta gaa aac gcc atg cgc caa atc att gaa gaa gaa aag 1305
Glu Ser Ala Leu Glu Asn Ala Met Arg Gln Ile Ile Glu Glu Glu Lys
405 410 415

att aaa gcg ggt agt ttt atg cag cct tta aga ttg gcc ctt ttg ggt 1353
Ile Lys Ala Gly Ser Phe Met Gln Pro Leu Arg Leu Ala Leu Leu Gly
420 425 430

aag gga ggc ggg ata ggc ctt aaa gaa gcg ctt ttt att tta ggc aaa 1401
Lys Gly Gly Gly Ile Gly Leu Lys Glu Ala Leu Phe Ile Leu Gly Lys
435 440 445 450

aca gag agc gtc aaa aga ata gag gat ttt ttg aaa aac taaaaaattg 1450
Thr Glu Ser Val Lys Arg Ile Glu Asp Phe Leu Lys Asn
455 460

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<212> PRT

<213> Helicobacter pylori

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20 25 30
Ala Asn Gln Gly Lys Phe Phe Leu Arg Ile Glu Asp Thr Asp Leu Ser
35 40 45
Arg Asn Ser Ile Glu Ala Ala Asn Ala Ile Ile Glu Ala Phe Lys Trp
50 55 60
Val Gly Leu Glu Tyr Asp Gly Glu Ile Leu Tyr Gln Ser Lys Arg Phe
65 70 75 80
Glu Ile Tyr Lys Glu Tyr Ile Gln Lys Leu Leu Asp Glu Asp Lys Ala
85 90 95
Tyr Tyr Cys Tyr Met Ser Lys Glu Glu Leu Asp Ala Leu Arg Glu Glu
100 105 110

Gln	Lys	Ala	Arg	Lys	Glu	Thr	Pro	Arg	Tyr	Asp	Asn	Arg	Tyr	Arg	Asp
		115					120					125			
Phe	Lys	Gly	Thr	Pro	Pro	Lys	Gly	Ile	Glu	Pro	Val	Val	Arg	Ile	Lys
		130				135					140				
Val	Pro	Gln	Asn	Glu	Val	Ile	Gly	Phe	Asn	Asp	Gly	Val	Lys	Gly	Glu
145				150					155						160
Val	Lys	Val	Asn	Thr	Asn	Glu	Leu	Asp	Asp	Phe	Ile	Ile	Ala	Arg	Ser
				165				170						175	
Asp	Gly	Thr	Pro	Thr	Tyr	Asn	Phe	Val	Val	Thr	Ile	Asp	Asp	Ala	Leu
			180				185					190			
Met	Gly	Ile	Thr	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Leu	Ser	Asn	Thr
		195					200				205				
Pro	Lys	Gln	Ile	Val	Leu	Tyr	Lys	Ala	Leu	Asn	Phe	Lys	Ile	Pro	Asn
		210				215					220				
Phe	Phe	His	Val	Pro	Met	Ile	Leu	Asn	Glu	Glu	Gly	Gln	Lys	Leu	Ser
225					230				235						240
Lys	Arg	His	Gly	Ala	Thr	Asn	Val	Met	Asp	Tyr	Gln	Glu	Met	Gly	Tyr
				245				250						255	
Leu	Lys	Glu	Ala	Leu	Val	Asn	Phe	Leu	Ala	Arg	Leu	Gly	Trp	Ser	Tyr
			260				265						270		
Gln	Asp	Lys	Glu	Val	Phe	Ser	Met	Gln	Glu	Leu	Leu	Glu	Leu	Phe	Asp
		275					280					285			
Pro	Lys	Asp	Leu	Asn	Ser	Ser	Pro	Ser	Cys	Phe	Ser	Trp	His	Lys	Leu
		290				295					300				
Asn	Trp	Leu	Asn	Ala	His	Tyr	Leu	Lys	Asn	Gln	Ser	Val	Gln	Glu	Leu
305					310					315					320
Leu	Lys	Leu	Leu	Lys	Pro	Phe	Ser	Phe	Ser	Asp	Leu	Ser	His	Leu	Asn
				325					330					335	
Pro	Thr	Gln	Leu	Asp	Arg	Leu	Leu	Asp	Ala	Leu	Lys	Glu	Arg	Ser	Gln
			340					345					350		
Thr	Leu	Lys	Glu	Leu	Ala	Leu	Lys	Ile	Asp	Glu	Val	Leu	Ile	Ala	Pro
		355					360					365			
Val	Glu	Tyr	Glu	Glu	Lys	Val	Phe	Lys	Lys	Leu	Asn	Gln	Ala	Leu	Val
		370				375					380				
Met	Pro	Leu	Leu	Glu	Lys	Phe	Lys	Leu	Glu	Leu	Asn	Lys	Ala	Asn	Phe
385					390					395					400
Asn	Asp	Glu	Ser	Ala	Leu	Glu	Asn	Ala	Met	Arg	Gln	Ile	Ile	Glu	Glu
				405					410					415	
Glu	Lys	Ile	Lys	Ala	Gly	Ser	Phe	Met	Gln	Pro	Leu	Arg	Leu	Ala	Leu
			420				425						430		
Leu	Gly	Lys	Gly	Gly	Gly	Ile	Gly	Leu	Lys	Glu	Ala	Leu	Phe	Ile	Leu
		435					440					445			
Gly	Lys	Thr	Glu	Ser	Val	Lys	Arg	Ile	Glu	Asp	Phe	Leu	Lys	Asn	
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<211> 382
<212> DNA
<213> Helicobacter pylori
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Met Phe
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56

aag ggg att tat cct atg cgt aat ttt cct atc cac cat aat ggt ttt 104
Lys Gly Ile Tyr Pro Met Arg Asn Phe Pro Ile His His Asn Gly Phe
5 10 15

aaa cat gaa gtg tta gct cac atg cta aaa agg cat aaa gag cca ttt 152
Lys His Glu Val Leu Ala His Met Leu Lys Arg His Lys Glu Pro Phe
20 25 30

att tta agc tat aat gac tgc gaa ttt gta agg aat gct tat aaa gat 200
Ile Leu Ser Tyr Asn Asp Cys Glu Phe Val Arg Asn Ala Tyr Lys Asp
35 40 45 50

ttt aaa att tta gaa cca tct tgg caa tac act atg gga caa ggc gag 248
Phe Lys Ile Leu Glu Pro Ser Trp Gln Tyr Thr Met Gly Gln Gly Glu
55 60 65

atc aga atg ggt aaa aat cgc tta gaa aga ggc gat aat aac cat gtc 296
Ile Arg Met Gly Lys Asn Arg Leu Glu Arg Gly Asp Asn Asn His Val
70 75 80

aaa caa tct cat gag tta ttg att atc aag gag taaaaatgca tattagcgaa 349
Lys Gln Ser His Glu Leu Leu Ile Ile Lys Glu
85 90

gtcaaaaactg ccttttaaaat cgctgatgta gaa 382

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<212> PRT
<213> Helicobacter pylori

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Gly Phe Lys His Glu Val Leu Ala His Met Leu Lys Arg His Lys Glu
20 25 30
Pro Phe Ile Leu Ser Tyr Asn Asp Cys Glu Phe Val Arg Asn Ala Tyr
35 40 45
Lys Asp Phe Lys Ile Leu Glu Pro Ser Trp Gln Tyr Thr Met Gly Gln
50 55 60
Gly Glu Ile Arg Met Gly Lys Asn Arg Leu Glu Arg Gly Asp Asn Asn
65 70 75 80
His Val Lys Gln Ser His Glu Leu Leu Ile Ile Lys Glu
85 90

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ataggggtga ttatagcatt tatggggcaa aaaaagtaga atctgtatca agttttatta 180
ag atg cat gcg gta aaa tcc gct aaa tca agg agt gtt att atg gaa 227

Met	His	Ala	Val	Lys	Ser	Ala	Lys	Ser	Arg	Ser	Val	Ile	Met	Glu		
1				5					10					15		
gca	gac	gca	acc	aca	cta	tta	gga	ttt	ttt	gaa	gaa	aat	caa	aac	aat	275
Ala	Asp	Ala	Thr	Thr	Leu	Leu	Gly	Phe	Phe	Glu	Glu	Asn	Gln	Asn	Asn	
			20					25					30			
caa	ttt	gtc	att	cct	atc	tat	cag	agg	ttg	tat	agt	tgg	aaa	aag	gaa	323
Gln	Phe	Val	Ile	Pro	Ile	Tyr	Gln	Arg	Leu	Tyr	Ser	Trp	Lys	Lys	Glu	
			35				40						45			
taatgcgaac	aattatggga	tgatattata	aaaattgggtg	ggaatgataa	gat											376
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Asp	Ala	Thr	Thr	Leu	Leu	Gly	Phe	Phe	Glu	Glu	Asn	Gln	Asn	Asn	Gln	
			20				25					30				
Phe	Val	Ile	Pro	Ile	Tyr	Gln	Arg	Leu	Tyr	Ser	Trp	Lys	Lys	Glu		
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					Met	Arg										
					1											
ctt	tat	caa	aaa	caa	ggc	ttg	gaa	atg	gtg	ggt	caa	aag	ttg	gat	tct	104
Leu	Tyr	Gln	Lys	Gln	Gly	Leu	Glu	Met	Val	Gly	Gln	Lys	Leu	Asp	Ser	
		5				10						15				
tat	tta	gcg	gat	aaa	tct	ttt	tgg	gca	gaa	gaa	ctt	caa	aac	aag	gac	152
Tyr	Leu	Ala	Asp	Lys	Ser	Phe	Trp	Ala	Glu	Glu	Leu	Gln	Asn	Lys	Asp	
	20				25						30					
acg	gat	ttt	ggc	tat	tat	caa	aac	aag	cag	ttt	tta	ttt	gtg	gct	aat	200
Thr	Asp	Phe	Gly	Tyr	Tyr	Gln	Asn	Lys	Gln	Phe	Leu	Phe	Val	Ala	Asn	
	35			40				45						50		
aaa	tcc	aag	ccc	agt	ttg	gag	ttt	tat	gag	ata	gaa	aat	aac	atg	ctt	248
Lys	Ser	Lys	Pro	Ser	Leu	Glu	Phe	Tyr	Glu	Ile	Glu	Asn	Asn	Met	Leu	
			55			60							65			
aaa	aaa	atc	aac	agc	tct	aaa	gct	ctt	gta	ggc	tct	aaa	aag	ggc	gat	296
Lys	Lys	Ile	Asn	Ser	Ser	Lys	Ala	Leu	Val	Gly	Ser	Lys	Lys	Gly	Asp	
		70				75							80			

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Lys Thr Leu Glu Gly Asp Leu Ala Thr Pro Ile Gly Val Tyr Arg Ile	
85 90 95	
acg cag aaa tta gag cgc ttg gat caa tat tat ggc gtt ttg gct ttt	392
Thr Gln Lys Leu Glu Arg Leu Asp Gln Tyr Tyr Gly Val Leu Ala Phe	
100 105 110	
gta acg aat tac cct aat ttg tat gat acc ttg aaa aaa cgc acc ggg	440
Val Thr Asn Tyr Pro Asn Leu Tyr Asp Thr Leu Lys Lys Arg Thr Gly	
115 120 125 130	
cat ggc att tgg gtg cat gga atg cct tta aat ggc gat cgg aat gaa	488
His Gly Ile Trp Val His Gly Met Pro Leu Asn Gly Asp Arg Asn Glu	
135 140 145	
ttg aac acc aag ggc tgt att gcg att gaa aac ccg ctt tta agc tct	536
Leu Asn Thr Lys Gly Cys Ile Ala Ile Glu Asn Pro Leu Leu Ser Ser	
150 155 160	
tat gac aaa gtg tta aaa ggc gaa aaa gcg ttc ctc atc acc tat gaa	584
Tyr Asp Lys Val Leu Lys Gly Glu Lys Ala Phe Leu Ile Thr Tyr Glu	
165 170 175	
gac aag ttt ttc cca agc acc aaa gaa gaa ttg agc atg att tta agc	632
Asp Lys Phe Phe Pro Ser Thr Lys Glu Glu Leu Ser Met Ile Leu Ser	
180 185 190	
tcc ctt ttt caa tgg aaa gaa gcc tgg gct agg ggc gat ttt gaa cgc	680
Ser Leu Phe Gln Trp Lys Glu Ala Trp Ala Arg Gly Asp Phe Glu Arg	
195 200 205 210	
tac atg cgt ttt tat aac ccc aat ttc act cgc tat gac ggc atg aaa	728
Tyr Met Arg Phe Tyr Asn Pro Asn Phe Thr Arg Tyr Asp Gly Met Lys	
215 220 225	
ttt aac gct ttt aaa gag tat aaa aaa agg gtg ttt gca aaa aac gaa	776
Phe Asn Ala Phe Lys Glu Tyr Lys Lys Arg Val Phe Ala Lys Asn Glu	
230 235 240	
aaa aag aat atc gct ttt tcc tct atc aat gtg atc cct tac ccc aac	824
Lys Lys Asn Ile Ala Phe Ser Ser Ile Asn Val Ile Pro Tyr Pro Asn	
245 250 255	
tct cag aac aaa cgc ttg ttt tat gtg gtg ttt gac caa gat tat aaa	872
Ser Gln Asn Lys Arg Leu Phe Tyr Val Val Phe Asp Gln Asp Tyr Lys	
260 265 270	
gcc tac cag cat aac aag ctc tct tat agc tcc aat tct caa aaa gaa	920
Ala Tyr Gln His Asn Lys Leu Ser Tyr Ser Ser Asn Ser Gln Lys Glu	
275 280 285 290	
ctc tat ata gag att gaa aac aat caa gtg tct att ata atg gaa aaa	968
Leu Tyr Ile Glu Ile Glu Asn Asn Gln Val Ser Ile Ile Met Glu Lys	
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54

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Lys Glu Gly Leu Gly Thr Arg Lys Lys Lys Asp Arg Ala Lys Lys Phe
245 250 255 260

ctg caa aaa tcc gca gaa ttt ggc tat gaa aaa gcc atg gaa gct ctg 870
Leu Gln Lys Ser Ala Glu Phe Gly Tyr Glu Lys Ala Met Glu Ala Leu
265 270 275

tagtttttta atcaaacttg tatcaagctt gactgaatgg gttagaaaaa tccgcttaga 930
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<211> 276
<212> PRT
<213> Helicobacter pylori

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Glu Tyr Ile Ser Ile Ser Asp Asp Trp Asp Glu Ile Val Arg Asn His
35 40 45
Lys Thr Tyr Tyr Phe Glu Asn Gly Leu Asp His Phe Asn Gln Gly Gln
50 55 60
Tyr Gln Gln Ala Phe Lys Asp Phe Arg Leu Ala Gln Glu Tyr Ser Ile
65 70 75 80
Gly Leu Gly Ser Val Tyr Leu Ala Lys Met Tyr Leu Glu Gly Lys Gly
85 90 95
Val Lys Val Asp Tyr Lys Lys Ala Gln Phe Tyr Ala Glu Asn Ala Ile
100 105 110
Lys Gly Tyr Gly Ser Gly Leu Leu Gly Gly Ala Leu Ile Leu Gly Arg
115 120 125
Met Gln Ala Glu Gly Leu Gly Met Lys Lys Asp Leu Lys Gln Ala Leu
130 135 140
Lys Thr Tyr Arg His Val Val Arg Met Phe Ser Asn Lys Ser Thr Asn
145 150 155 160
Phe Ala Asn Asn Phe Arg Leu Pro Asn Leu Ala Glu Phe Thr Ser Met
165 170 175
Leu Ile Gly Ser Arg Phe Ile Asp Leu Ser Gly Leu Ser Ala Asn Pro
180 185 190
Ile Lys Phe Gly Lys Lys Phe Gly Ile Leu Val Lys Lys Ser Thr Gln
195 200 205
Ile Lys Asp Lys Thr Leu Leu Trp Glu Asp Ile Ala Glu Ile Ser Ser
210 215 220
Asn Ile Thr Leu Leu Lys Gln Gln Met Gly Glu Ile Leu Tyr Arg Ile
225 230 235 240
Gly Ile Ala Tyr Lys Glu Gly Leu Gly Thr Arg Lys Lys Lys Asp Arg
245 250 255
Ala Lys Lys Phe Leu Gln Lys Ser Ala Glu Phe Gly Tyr Glu Lys Ala
260 265 270
Met Glu Ala Leu
275

<210> 357
<211> 2685

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aat Asn 225	gaa Glu	gaa Glu	gaa Glu	aga Arg	aaa Lys 230	gca Ala	tgt Cys	ctt Leu	aaa Lys	aat Asn 235	ctc Leu	cct Pro	aaa Lys	gac Asp	tta Leu 240	720
cag Gln	gaa Glu	aat Asn	att Ile	tta Leu 245	gct Ala	aaa Lys	gag Glu	agt Ser	ctt Leu 250	aaa Lys	gct Ala	tat Tyr	aaa Lys	gac Asp 255	tgc Cys	768
ctc Leu	tct Ser	caa Gln	gct Ala 260	aga Arg	aat Asn	gaa Glu	gaa Glu	gaa Glu 265	agg Arg	aga Arg	gct Ala	tgc Cys	gag Glu 270	aaa Lys	cta Leu	816
ctc Leu	acg Thr	cct Pro 275	gaa Glu	gcg Ala	aga Arg	aaa Lys	ctc Leu 280	tta Leu	gag Glu	caa Gln	gaa Glu 285	gtt Val	aag Lys	aaa Lys	agc Ser	864
gtt Val 290	aag Lys	gct Ala	tat Tyr	ttg Leu	gac Asp	tgc Cys 295	gta Val	tca Ser	aga Arg	gct Ala	agg Arg 300	aat Asn	gaa Glu	aaa Lys	gag Glu	912
aaa Lys 305	aaa Lys	gaa Glu	tgc Cys	gag Glu	aaa Lys 310	tta Leu	ctc Leu	acg Thr	cct Pro	gaa Glu 315	gcg Ala	aga Arg	aaa Lys	ttt Phe	tta Leu 320	960
gcg Ala	aaa Lys	gaa Glu	ctc Leu	caa Gln 325	caa Gln	aaa Lys	gat Asp	aaa Lys	gcg Ala 330	atc Ile	aaa Lys	gat Asp	tgc Cys	ttg Leu 335	aaa Lys	1008
aac Asn	gcc Ala	gat Asp	cct Pro 340	aac Asn	gac Asp	aga Arg	gcg Ala	gct Ala 345	atc Ile	atg Met	aag Lys	tgt Cys	ttg Leu 350	gat Asp	ggt Gly	1056
ttg Leu	agc Ser	gat Asp 355	gaa Glu	gag Glu	aag Lys	ctc Leu	aaa Lys 360	tac Tyr	ctg Leu	caa Gln	gaa Glu 365	gct Ala	aga Arg	gaa Glu	aag Lys	1104
gct Ala	gtt Val 370	gcg Ala	gat Asp	tgt Cys	ttg Leu	gct Ala 375	atg Met	gct Ala	aaa Lys	acc Thr	gat Asp 380	gaa Glu	gaa Glu	aaa Lys	agg Arg	1152
aaa Lys 385	tgc Cys	caa Gln	aac Asn	ctt Leu	tat Tyr 390	agc Ser	gat Asp	ttg Leu	atc Ile	caa Gln 395	gaa Glu	atc Ile	caa Gln	aat Asn	aaa Lys 400	1200
agg Arg	aca Thr	caa Gln	aac Asn	aaa Lys 405	caa Gln	aat Asn	caa Gln	ttg Leu	agt Ser 410	aaa Lys	aca Thr	gaa Glu	agg Arg	ttg Leu 415	cat His	1248
caa Gln	gca Ala	agc Ser	gag Glu 420	tgc Cys	ttg Leu	gat Asp	aac Asn	tta Leu 425	gat Asp	gac Asp	cct Pro	act Thr	gat Asp 430	caa Gln	gag Glu	1296
gcc Ala	ata Ile	gag Glu	caa Gln	tgt Cys	tta Leu	gag Glu	ggc Gly	ttg Leu	agc Ser	gat Asp	agt Ser	gaa Glu	agg Arg	gcg Ala	cta Leu	1344

435	440	445	
att cta gga att aaa cga caa gct gat gaa gtg gat ctg att tat agc Ile Leu Gly Ile Lys Arg Gln Ala Asp Glu Val Asp Leu Ile Tyr Ser 450 455 460			1392
gat cta aga aac cgt aaa acc ttt gat aac atg gcg gct aaa ggt tat Asp Leu Arg Asn Arg Lys Thr Phe Asp Asn Met Ala Ala Lys Gly Tyr 465 470 475 480			1440
cca ttg tta cca atg gat ttc aaa aat ggc ggc gat att gcc act att Pro Leu Leu Pro Met Asp Phe Lys Asn Gly Gly Asp Ile Ala Thr Ile 485 490 495			1488
aac gcc act aat gtt gat gcg gac aaa ata gct agc gat aat cct att Asn Ala Thr Asn Val Asp Ala Asp Lys Ile Ala Ser Asp Asn Pro Ile 500 505 510			1536
tat gct tcc ata gag cct gat att gcc aag caa tac gaa aca gaa aaa Tyr Ala Ser Ile Glu Pro Asp Ile Ala Lys Gln Tyr Glu Thr Glu Lys 515 520 525			1584
acc att aag gat aag aat tta gaa gct aaa tta gct aag gct tta ggt Thr Ile Lys Asp Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala Leu Gly 530 535 540			1632
ggc aat aaa aaa gat gac gat aaa gaa aaa agt aaa aaa tcc aca gca Gly Asn Lys Lys Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser Thr Ala 545 550 555 560			1680
gaa gct aaa gca gaa aac aat aag ata gac aaa gat gtc gca gaa act Glu Ala Lys Ala Glu Asn Asn Lys Ile Asp Lys Asp Val Ala Glu Thr 565 570 575			1728
gcc aag aat atc agt gaa atc gct ctt aag aac aaa aaa gaa aag agt Ala Lys Asn Ile Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu Lys Ser 580 585 590			1776
ggg gaa ttt gta gat gaa aat ggt aat ccc att gat gac aaa aag aaa Gly Glu Phe Val Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys Lys Lys 595 600 605			1824
gca gaa aaa caa gat gaa aca agc cct gtc aaa cag gcc ttt ata ggc Ala Glu Lys Gln Asp Glu Thr Ser Pro Val Lys Gln Ala Phe Ile Gly 610 615 620			1872
aag agt gat ccc aca ttt gtt tta gcg caa tac acc ccc att gaa atc Lys Ser Asp Pro Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile Glu Ile 625 630 635 640			1920
act ctg act tct aaa gta gat gcc act ctc aca ggt ata gtg agt ggg Thr Leu Thr Ser Lys Val Asp Ala Thr Leu Thr Gly Ile Val Ser Gly 645 650 655			1968
gtt gta gcc aaa gat gta tgg aac atg aac ggc act atg atc tta tta Val Val Ala Lys Asp Val Trp Asn Met Asn Gly Thr Met Ile Leu Leu 660 665 670			2016
gac aaa ggc act aag gtg tat ggg aat tat caa agc gtg aaa ggt ggc			2064

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Thr	Pro	Ile	Met	Thr	Arg	Leu	Met	Ile	Val	Phe	Thr	Lys	Ala	Ile	Thr		
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Pro	Asp	Gly	Val	Ile	Ile	Pro	Leu	Ala	Asn	Ala	Gln	Ala	Ala	Gly	Met		
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Arg	Ile	Gly	Phe	Ala	Val	Ile	Ala	Ser	Val	Val	Asn	Ser	Phe	Leu	Gln		
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Arg	Ser	Glu	Arg	Thr	Pro	Glu	Phe	Asn	Tyr	Ala	Leu	Gly	Gln	Ala	Ile		
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caa	ctg	atg	aat	atc	ccc	cca	agt	ttt	tac	aaa	aac	gag	ggc	gat	agt	2448	
Gln	Leu	Met	Asn	Ile	Pro	Pro	Ser	Phe	Tyr	Lys	Asn	Glu	Gly	Asp	Ser		
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Val	Lys	Ile	Thr	Asn	Lys	Ser	Val	Val	Asp	Glu	Ile	Ile	Lys	Gln	Ser		
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Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Ala	Lys
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Glu	Ser	Val	Lys	Ala	Tyr	Lys	Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu
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Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys
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Ala	Asp	Lys	Lys	Arg	Cys	Val	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Lys
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Lys	Val	Leu	Ala	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser
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Arg	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr
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Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Leu	Lys	Ala
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Tyr	Lys	Asp	Cys	Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala
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Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu
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Val	Lys	Lys	Ser	Ile	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg
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Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala
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Arg	Lys	Phe	Leu	Ala	Lys	Gln	Val	Leu	Asn	Cys	Leu	Glu	Lys	Ala	Gly
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Gln	Glu	Asn	Ile	Leu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys
			245						250					255	
Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala	Cys	Glu	Lys	Leu
			260					265					270		
Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu	Val	Lys	Lys	Ser
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Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu
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Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Phe	Leu
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Ala	Lys	Glu	Leu	Gln	Gln	Lys	Asp	Lys	Ala	Ile	Lys	Asp	Cys	Leu	Lys
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Asn	Ala	Asp	Pro	Asn	Asp	Arg	Ala	Ala	Ile	Met	Lys	Cys	Leu	Asp	Gly
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Leu	Ser	Asp	Glu	Glu	Lys	Leu	Lys	Tyr	Leu	Gln	Glu	Ala	Arg	Glu	Lys
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Ala	Val	Ala	Asp	Cys	Leu	Ala	Met	Ala	Lys	Thr	Asp	Glu	Glu	Lys	Arg
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Lys	Cys	Gln	Asn	Leu	Tyr	Ser	Asp	Leu	Ile	Gln	Glu	Ile	Gln	Asn	Lys
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Arg	Thr	Gln	Asn	Lys	Gln	Asn	Gln	Leu	Ser	Lys	Thr	Glu	Arg	Leu	His
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Gln	Ala	Ser	Glu	Cys	Leu	Asp	Asn	Leu	Asp	Asp	Pro	Thr	Asp	Gln	Glu
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Asp	Leu	Arg	Asn	Arg	Lys	Thr	Phe	Asp	Asn	Met	Ala	Ala	Lys	Gly	Tyr

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Tyr	Ala	Ser	Ile	Glu	Pro	Asp	Ile	Ala	Lys	Gln	Tyr	Glu	Thr	Glu	Lys
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Glu	Ala	Lys	Ala	Glu	Asn	Asn	Lys	Ile	Asp	Lys	Asp	Val	Ala	Glu	Thr
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Gly	Glu	Phe	Val	Asp	Glu	Asn	Gly	Asn	Pro	Ile	Asp	Asp	Lys	Lys	Lys
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Ala	Glu	Lys	Gln	Asp	Glu	Thr	Ser	Pro	Val	Lys	Gln	Ala	Phe	Ile	Gly
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		675					680					685			
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	690					695					700				
Pro	Asp	Gly	Val	Ile	Ile	Pro	Leu	Ala	Asn	Ala	Gln	Ala	Ala	Gly	Met
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Leu	Gly	Glu	Ala	Gly	Val	Asp	Gly	Tyr	Val	Asn	Asn	His	Phe	Met	Lys
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Thr	Ala	Pro	Ile	Ile	Ala	Leu	Asp	Lys	Leu	Ile	Gly	Leu	Gly	Lys	Gly
		755				760					765				
Arg	Ser	Glu	Arg	Thr	Pro	Glu	Phe	Asn	Tyr	Ala	Leu	Gly	Gln	Ala	Ile
	770					775					780				
Asn	Gly	Ser	Met	Gln	Ser	Ser	Ala	Gln	Met	Ser	Asn	Gln	Ile	Leu	Gly
785					790					795					800
Gln	Leu	Met	Asn	Ile	Pro	Pro	Ser	Phe	Tyr	Lys	Asn	Glu	Gly	Asp	Ser
			805						810					815	
Ile	Lys	Ile	Leu	Thr	Met	Asp	Asp	Ile	Asp	Phe	Ser	Gly	Val	Tyr	Asp
		820						825					830		
Val	Lys	Ile	Thr	Asn	Lys	Ser	Val	Val	Asp	Glu	Ile	Ile	Lys	Gln	Ser
		835					840					845			
Thr	Lys	Thr	Leu	Ser	Arg	Glu	His	Glu	Glu	Ile	Thr	Thr	Ser	Pro	Lys
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aat gaa att gaa tta gcc ctt att aga ggc gat gag gac gct aaa gaa	157
Asn Glu Ile Glu Leu Ala Leu Ile Arg Gly Asp Glu Asp Ala Lys Glu	
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atc tta gaa aaa aga ttg gat aag gag gtt aaa agc att tat tcc aat	205
Ile Leu Glu Lys Arg Leu Asp Lys Glu Val Lys Ser Ile Tyr Ser Asn	
35 40 45	
ctc act gat ttt caa aaa ctc caa tta gca aga cac cct gac aga ccc	253
Leu Thr Asp Phe Gln Lys Leu Gln Leu Ala Arg His Pro Asp Arg Pro	
50 55 60	
tac gct atg gat tac att gat ctc atc tta aaa gat aaa tat gaa gtc	301
Tyr Ala Met Asp Tyr Ile Asp Leu Ile Leu Lys Asp Lys Tyr Glu Val	
65 70 75	
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Phe Gly Asp Arg His Tyr Asn Asp Asp Lys Ala Ile Val Cys Phe Val	
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Gly Lys Ile Asp Asn Val Pro Val Val Val Ile Gly Glu Glu Lys Gly	
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Arg Gly Thr Lys Asn Lys Leu Leu Arg Asn Phe Gly Met Pro Asn Pro	
115 120 125	
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Cys Gly Tyr Arg Lys Ala Leu Lys Met Ala Lys Phe Ala Glu Lys Phe	
130 135 140	
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Asn Leu Pro Ile Leu Met Leu Val Asp Thr Ala Gly Ala Tyr Pro Gly	
145 150 155	
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Ile Gly Ala Glu Glu Arg Gly Gln Ser Glu Ala Ile Ala Lys Asn Leu	
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caa gag ttc gcc tct tta aaa gtc cct act att tct gta att atc ggt	637
Gln Glu Phe Ala Ser Leu Lys Val Pro Thr Ile Ser Val Ile Ile Gly	
180 185 190	
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Glu Gly Gly Ser Gly Gly Ala Leu Arg Leu Gln Trp Leu Thr Asn Trp	
195 200 205	
cta tgatggaata ttccattttt agcgttatat cccagaagg ttgtgcggcg	738
attctttggg atgaccctag caagactgaa gtggctatta aagcgatgaa aatcacgcct	798
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Leu	Glu	Lys 35	Arg	Leu	Asp	Lys	Glu 40	Val	Lys	Ser	Ile	Tyr 45	Ser	Asn	Leu
Thr	Asp 50	Phe	Gln	Lys	Leu 55	Gln	Leu	Ala	Arg	His 60	Pro	Asp	Arg	Pro	Tyr
Ala 65	Met	Asp	Tyr	Ile 70	Asp	Leu	Ile	Leu	Lys	Asp 75	Lys	Tyr	Glu	Val	Phe 80
Gly	Asp	Arg	His 85	Tyr	Asn	Asp	Asp	Lys	Ala 90	Ile	Val	Cys	Phe 95	Val	Gly
Lys	Ile	Asp	Asn 100	Val	Pro	Val	Val	Val 105	Ile	Gly	Glu	Glu	Lys 110	Gly	Arg
Gly	Thr	Lys 115	Asn	Lys	Leu	Leu	Arg	Asn 120	Phe	Gly	Met	Pro	Asn 125	Pro	Cys
Gly	Tyr 130	Arg	Lys	Ala	Leu	Lys 135	Met	Ala	Lys	Phe 140	Ala	Glu	Lys	Phe	Asn
Leu 145	Pro	Ile	Leu	Met 150	Leu	Val	Asp	Thr	Ala	Gly 155	Ala	Tyr	Pro	Gly	Ile 160
Gly	Ala	Glu	Glu	Arg 165	Gly	Gln	Ser	Glu	Ala 170	Ile	Ala	Lys	Asn 175	Leu	Gln
Glu	Phe	Ala	Ser 180	Leu	Lys	Val	Pro	Thr 185	Ile	Ser	Val	Ile	Ile 190	Gly	Glu
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Met	Gln	Phe	Thr	Gly	Lys	Asn	Val	Leu	Ile	Thr	Gly	Ala	Ser			
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aaa	ggc	att	ggg	gct	gaa	atc	gcc	aaa	act	ctc	gct	tct	atg	ggg	ctg	156
Lys	Gly	Ile	Gly	Ala	Glu	Ile	Ala	Lys	Thr	Leu	Ala	Ser	Met	Gly	Leu	
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Lys	Val	Trp	Ile	Asn	Tyr	Arg	Ser	Asn	Ala	Glu	Val	Ala	Asp	Ala	Leu	
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Arg Leu
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373

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23

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24

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32

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33

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